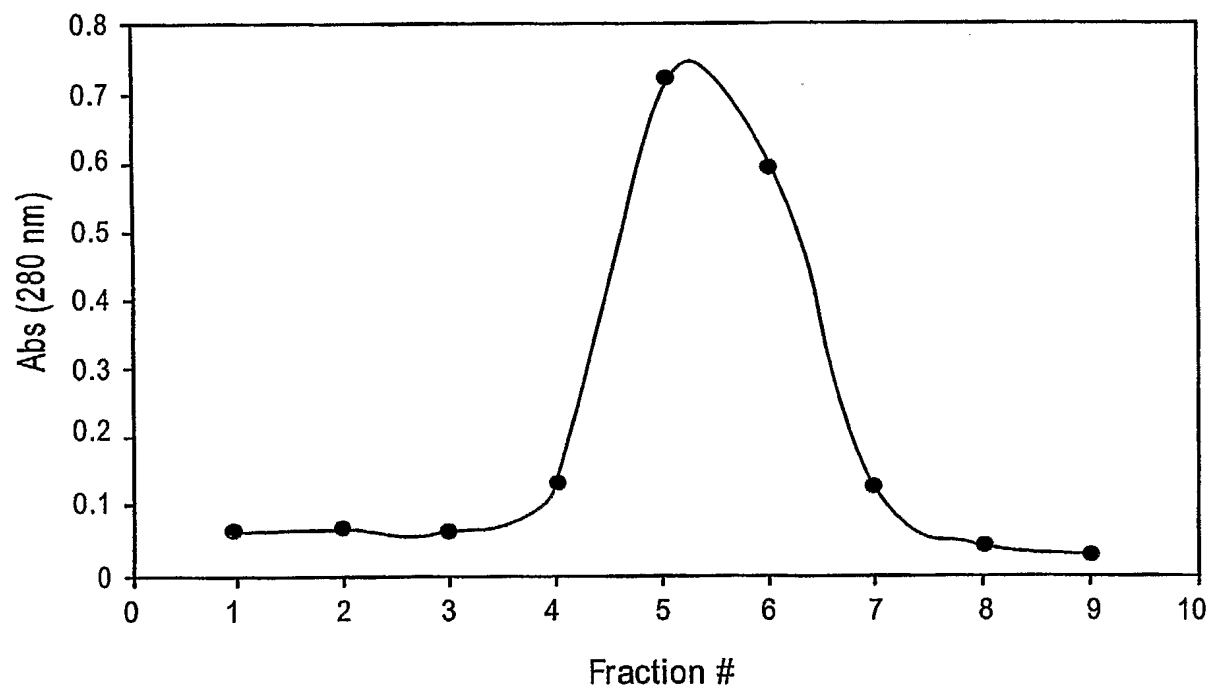


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	1 mM	0.1 mM	0.3 mM	mM	mM	0.055%	550 mM	1.1 mM	2.2 mM	2.2 mM	CaCl ₂	440 mM	550 mM	Activity
#	GSH	GSSG	LM	NaCl	KCl	PEG 3350	GndHCl	EDTA	MgCl ₂			Sucrose	L- Arg	U/g IB
2 (55 mM MES pH 6.5)	+	+	+	10.56	0.44	0	+	0	+		+	0	0	0
3 (55 mM MES pH 6.5)	+	+	0	10.56	0.44	+	+	+	0		0	+	+	0
#5 (55 mM MES pH 6.5)	+	+	0	264	11	0	0	0	+		+	+	0	0
#8 (55 mM MES pH 6.5)	+	+	+	264	11	+	0	+	0		0	0	+	40.00
#10 (55 mM MES pH 8.2)	+	+	+	10.56	0.44	0	0	+	0		0	+	0	0
#11 (55 mM Tris pH 8.2)	+	+	0	10.56	0.44	+	0	0	+		+	0	+	105.26
#13 (55 mM Tris pH 8.2)	+	+	0	264	11	0	+	+	0		0	0	0	15.65
#16 (55 mM Tris pH 8.2)	+	+	+	264	11	+	+	0	+		+	+	+	48.70

FIG. 1

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ELution of MBP-ST3Gal III from Amylose column**FIG. 2**

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**ST3 Gal III activities of the Amylose purified
refolded MBP-ST3Gal III fractions**

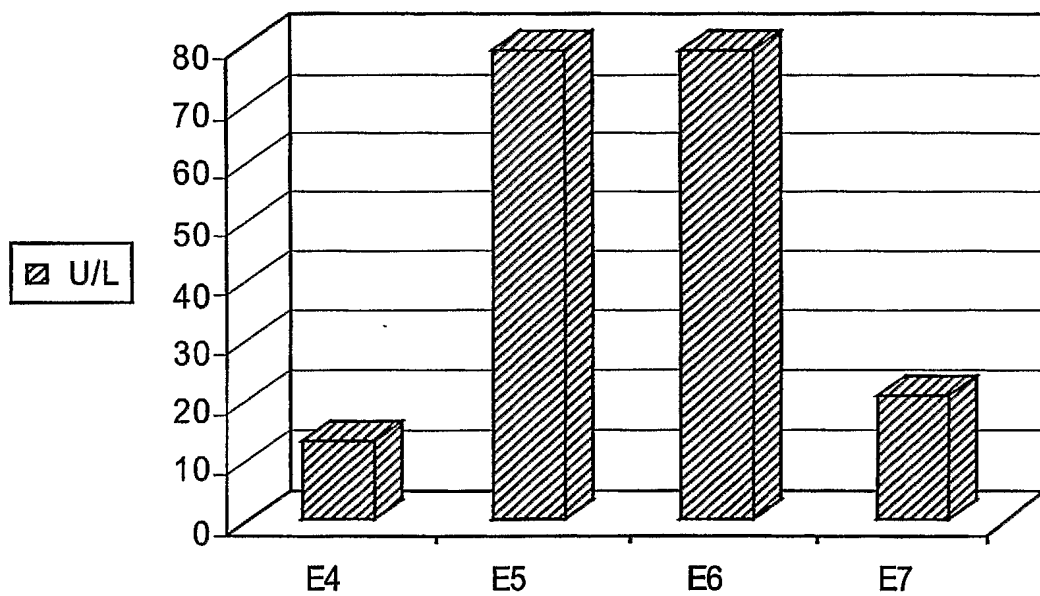
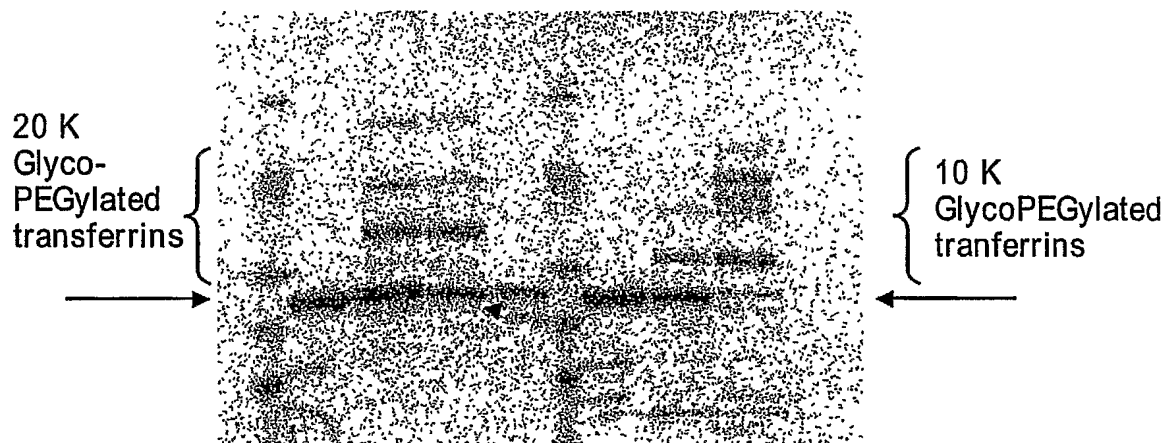
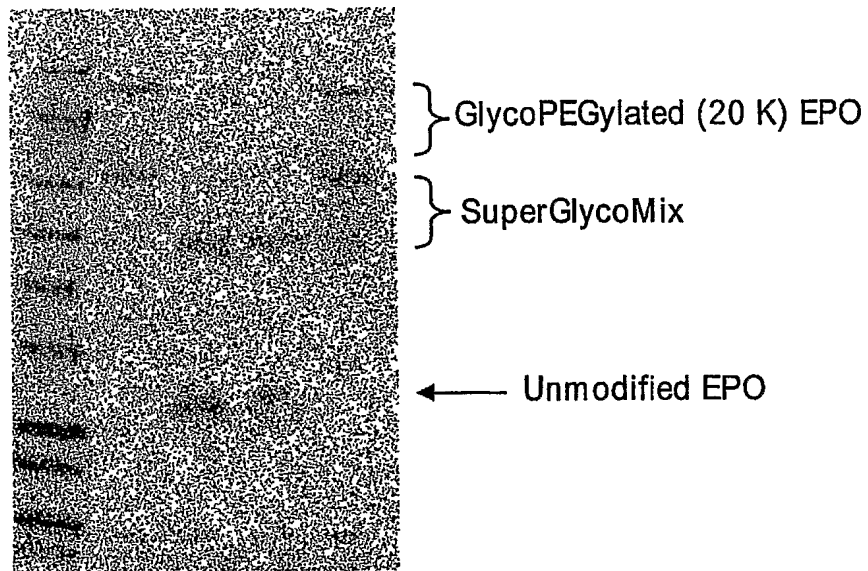


FIG. 3

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**FIG. 4**

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GlycoPEGylation (20 K) of EPO

FIG. 5

10 20 30 40 50 60
/usr/t MLKKQSAGLV LWGAILF VAWNALL LLLFFWTRPAPGRPPSVSALDGD PASLTREVI RLAQD
::: :::
P27115 MLKKQSAGLV LWGAILF VAWNALL LLLFFWTRPVPSRL PSDNALDDDPASLTREVI RLAQD
10 20 30 40 50 60

70 80 90 100 110
/usr/t AEVELERQRGLLQQIGD--ALSSQRGRVPTA APPAQPRVPVTPAPA VIPILVIACDRSTV
::: :
P27115 AEVELERQRGLLQQIREH HALWSQRWKVPTA APPAQPHVPVTPPPAVIPILVIACDRSTV
70 80 90 100 110 120

120 130 140 150 160 170
/usr/t RRCLDKLLHYRPSAE LFPIIVSQDCGHEETAQA IASYGS AVTHIRQPDLSSI AVPPDHRK
::: :::
P27115 RRCLDKLLHYRPSAE LFPIIVSQDCGHEETAQV IASYGS AVTHIRQPDL SNI AVQP DHRK
130 140 150 160 170 180

180 190 200 210 220 230
/usr/t FQGY YKIARHYRWAL GQVFRQRFPA AVVVEDDLEVA PDFFEYFRATYP LLKADPSL WCV
::: :::
P27115 FQGY YKIARHYRWAL GQIFHNFNYPAA VVVEDDLEVA PDFFEYFOATYP LLKADPSL WCV
190 200 210 220 230 240

240 250 260 270 280 290
/usr/t SAWNDNGKEQMVDASRP ELLYRTDFFPGLGWILL LAELWAELEPKWP KAFWDDWMRRPEQR
::: :::
P27115 SAWNDNGKEQMVDSSKP ELLYRTDFFPGLGWILL LAELWAELEPKWP KAFWDDWMRRPEQR
250 260 270 280 290 300

300 310 320 330 340 350
/usr/t QGRACIRPEISR TMTFGRKGVS HGOFFDQH LKFIKLNQQF VHFTQLDLSYLQ REAYDRDF
::: :::
P27115 KGRACVRPEISR TMTFGRKGVS HGOFFDQH LKFIKLNQQF VPFTQLDLSYLQ QEAYDRDF
310 320 330 340 350 360

360 370 380 390 400 410
/usr/t IARVYGAPQLQVEKV RTNDRKELGE VRVQYTGRDSFKAF AKALGVMD DLKSGVPRAGYRG
::: :::
P27115 IARVYGAPQLQVEKV RTNDRKELGE VRVQYTGRDSFKAF AKALGVMD DLKSGVPRAGYRG
370 380 390 400 410 420

420 430 440
/usr/t IVTFQFRGRRVHLAPP PTWEGYDPSWN
::::
P27115 IVTFLFRGRRVHLAPP QTWDGYDPSWT
430 440

FIG. 6

FIG. 6

GnT1 Cys121Ser mutant

avipilviacdrstvrslldkllhyrpsaelpiivsqdcgheetaqaiaysgavthirqpdlssiavpdpdhrkfqgyyklarhyrwa
lgqvfrqfrfpaavvddlevapdffeyfratypllkadpslwcvsawndngkeqmvdasrpellyrtdffpgllawlaelwae
lepkwpkafwddwmirpeqrqgracirpeisrmtufgrkgvshgqffdqhlkfiklnqqfvhftqlldslqlreaydrdfllaryyg
apqlqvekvrtndrkelgevrvqytrgdsfkafaklgvmdllksgvpragyrvgtvfqfpgtrrvhlappptwgydpswn*

[illegible]

FIG. 7

GnT1 Cys121Asp

avipilviacdrstvrrdlkllhrypsaelpiivsqdcgheetaqaiasygsavthirqpdlssiavpdpdhrkfqgyykiarhyrwa
lgqvfrqfrfpaavvveddleavpddfeyfratypllkdpshvcvsawndngkeqmvdasrpellyrtdffpqlgwillaelwae
lepkwpkafwdwmrpeqrqgracirpeisrmtfgrkgvshgqffdqlhkfiknqcfvhtqldlsylqreaydrdflaryyg
apqlqavekvtndrkelgevrvyqtrgdsfkafakalgvmdllksgvpragyrvitvfqpgtrvhlappptwgydpswn*

[illegible]

GE

GnT1 Cys121Thr

avipilviacdrstvrtdkllyrpsaelfpivsqdcgheetaiaasygsavthirqpdlssiaavppdhrkfqggykiahryrwal
 gqvfrqfrfpaavvveddleavapdfeyfratypillkadpslwcvswndngkeqmvdasrpellyrtdffpgllwllaelwael
 epkwpkafwdwmrpeqrqgracirpeisrmtfgrkgvshgqffdqhlkfiklnqqfwhftqlldsllylqreaydrdflarvyg
 apqlqvekvtrndrkelgevrqvtygrdsfkafakalgvmddllksgvpragrygvtvtfqfpgrrvhlappptwegydpawn*

Gcgggtgattcccatccttggtcatcgcctgtgaccgcagcactgttcggcgcaactctagacaagctgctgcattatcgccctcggcctg
 agctcttcccatcatcgttagccaggaactgcgggcacgagagagacggcccgagggccatcgcctctacggcagcggcggcgcac
 atcgggcagcccgacctgagcagcattgcgggtgcgcgggaaccacccgcaagttccaggggctactacaaagatcggcggccactacc
 gctgggcgcctggggccaggctctccggcagtttcgcttcccgccggcgcgtggtggagggatgacctggagggcggcggcggcggcgttct
 tcgaggtacttccggggccaccctatccgctgctgaaggccgacccctccctgtgtgtgcgtctcggccttggaatgacaaaggcgaaggagc
 agatgggtggacggcagcaggccctgagctgctctaccgcaccgaccttttccctggcctgggcctgtgctgtgtggcggcggcggc
 tgaagctggagagcccaaggcccttctggggacgactgggatggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc
 gcccctgagatctcaagaacgatgaccttggccgcaagggtgtgagccacggggcagttctttgacacagcaccctcaagtttatcaaggctg
 aaaccagcagtttggcacttcaccacagctggacctgttacctgacagcgggagggccctatgaccggagatttccctcggcggcgtctacggg
 tgcctcccccagctgcaagggtggagaaagtggagaccacgaaggagctggggggaggtgcgggtgcaggtatcacggggcagggga
 cagcttcaaggccttcccaaggcctcgtgggtgctcatggtgacctaagtcgggggggttccgagagctgggtaccgggggtattgtcacctt
 ccaggttccggggccggcgtgtccacctggcggcccccaccgacgtggggaggggctatgatcctagctgggaattag

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FIG. 9

GnT1 Cys121Ala

avipilviacdrstvrraldklhlyrpsaelfpriivsqdcgheetaqaiasygsavthirqpdlssiavppdhrkfggyykiarhyrwa
 lgqvfrqfrfpaavvveddleavpddfeyfratypilkadpsslwcvswndngkeqmvdasrpellyrtdffpglgwllaelwae
 lepkwpkafwddwmrpeqrgracirpeisrntnftgrkgvshgqffdqhlkfiklnqfwhftqldsylqreaydrdrflarvyg
 apqlqvekvtrndrkclgevrqvtygrdsfkafakalgvmddllksvpragrygvtqfpgrrvhlappptwegydpawn*

Gcgggtattccatccttggtcatcgccctgtgacccgcagcactgttcggcggcccttagacaagctgctgcattatcgccctcggctg
 agctcttccccatcatcggttagccaggactgcggggcacgagggagacggcccgagggccatcgccctctctacggcgagcggtcacggcac
 atccggcagccccgacctgagcagcattgcgggtgcccggaccacggcaagtccagggtctactacaagatcgccggccactacc
 gctggggcgcgtggggccaggctcttccggcaggtttcgcttccccggccggcggcgtggtggggaggatgacctggagggtggccccgggacttct
 tcgagttactttcggggccaccatccgctgctgaaaggccgagccccctccctgtgggtgctctggcctgggaatgacaacgggcaaggaggc
 agatgggtggagggccagcaggcctgaggctgctctacccgacggacttttttccctgggctgggctgggctggtgtgtggccggagctctggggc
 tggagctggagggcccaaggctggccaaaggcccttctggggacgactggatggcggccggccggcagcagcgccggggccctggcatatc
 gcccctggagatctcaagaacgatgaccttggccgcaagggtgtgagccacggggcagttcttggaccagcaacctcaagtattatcaaggctg
 aaccaggcaggttggcacttcaaccagctggagcctgtcttaccttgacggaggccctatgacccaggatttctcggcccgctctacggg
 tgcctcccaggctggcagggtggagaaagtggagaccatgacccggaaaggagctggggggaggtgtgcgggtgcaggtatatacggggcaggsga
 cagcttcaaggcttccgcaaggctctgggtgtcatggatgaccttaagtcgggggttccggaggctgggtaccgggggtattgtcacctt
 ccagttccccggggccgctgtgtccaccctggcggccccccacccagcagtgaggggctatgatcctagctgggaattag

FIG. 10

GnT1 Arg120Ala, Cys121H

avipilviacdrstvra**h**ldkllyrpsaelfpivsqdcgheetaqaiasygsavthirqpdlssiaavppdhrkfqggyykiarhyrw
 algqvfrqfrfpaavvveddleavdpdffeyfratypllkadpslwcvsawndngkeqmvdasrpellyrtddffpglgwlllaelwa
 elepkwpkafwddwnrrpeqrqgracirpeisrmtfgrkgsghqffdqhlkfiklnqqfvhfqlldlsylqreaydrdrflarvy
 gapqlqvekvrtndrkelgevrqvtygrdsfkafakalgvmddllksgvpragyivtfqfpgirrvhlappptwegydpwswn*

Gcgggtgattcccatcctgtgtcatcgcctgtgaccgcagcacactgttcggggccacccctagacaagctgtgcattatcggccctcggcctg
 agctcttcccatcatcgttagccagagactgcgggcacagagagagacggccagggccatcgcctctactacggcagcggcggcgcacac
 atccggcagcccgacactgagcagcattggcgggtgcggccgggacaccgcgaagttccaggsggtactacaagatcggcggccactacc
 gctggggcgcctggggccagggtctccggcagtttcgcttcccccggcgcgtgtgtggaggatgacctggagggtggccccggacttct
 tcgagttacttccggggccacctatccgctgtgaaaggccgacccctccctgtgtgtcgtctcggccttggaatgacaacgggcaaggagc
 agatgtgtggacggcagagccctgagctgtctctaccgcaccgacttttccctggcctggggctggcctgtgtggcggcaggctctggsgc
 tggagctggagagcccaagtgcccaaggccctctggggacgactggatggcggcggccggagcagcggcagsgsgcgggctgcatac
 gcccgtgagatctcaagaacgatgaccttggccggcaaggsgtgtgagccacggggcagttctttgaccacgacacctcaagtttatcaagctg
 aaaccagcagtttgtgacacttaccacagctgggacctgtcttacctgacagcgggagggcctatgaccggagatttccctcggccgctctacggg
 tgttccccagctgcaagggtggagaaagtggagaccacgggagagagctggggggaggggtgcggsgtagtatacggsgcagggga
 cagcttcaaggccttcccaaggcctctgggtgtcatggatgacctaagtcgggggttccggagagctggctaccgggggtattgtcacctt
 ccagttccggggcgcggctgtccacctggcggcccccacccagcgtggggaggggctatgatcctagctgggaattag

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FIG. 11

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Rat Liver ST3Gal III amino acid sequence:

MGLLVFVRNLLALCLFELVLGFLYYSAWKLHLLQWEDSNLSLILSLDSAGQTLGTEYDRL
 GFLLKLD SKLP AELATKYANFSEGACKPGYASAMMTAIFPRFSKPAPMFLDSDSFRKW
 ARIRFVPPFGIKGQDNLIKAILSVTKEYRLTPALDSLHCRRCCIIVGNGGVLANKSLGS
 RIDDDYDIVIRLNSAPVKGFEKDVGSKTTTLRITYPEGAMQRPQYERDSLFVLAGFKW
 QDFKWLKYIVYKERVASDGFVKSVATRVPKPEPEIRILNPYFIQEAFTLIGLPFNN
 GLMGRGNIPTLGSAVVTMALDGCDEVAVAGFGYDMNTPNAPLHYHYYETVRMAAIKE
 SWTHNIQREKEFLRKLVKARVITDLSGGI

FIG. 12

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Full length UDP-N-acetylgalactosaminyltransferase 2 (GalNAcT2)

nucleic acid and amino acid sequences

Amino acid sequence

Met 1	Arg	Arg	Arg	Arg	Ser 5	Arg	Met	Leu	Leu	Cys 10	Phe	Ala	Phe	Leu	Trp 15	Val
Leu	Gly	Ile	Ala 20	Tyr	Tyr	Met	Tyr	Ser 25	Gly	Gly	Gly	Ser	Ala 30	Leu	Ala	
Gly	Gly	Ala 35	Gly	Gly	Gly	Ala	Gly 40	Arg	Lys	Glu	Asp	Trp 45	Asn	Glu	Ile	
Asp	Pro 50	Ile	Lys	Lys	Lys	Asp 55	Leu	His	His	Ser	Asn 60	Gly	Glu	Glu	Lys	
Ala 65	Gln	Ser	Met	Glu	Thr 70	Leu	Pro	Pro	Gly	Lys 75	Val	Arg	Trp	Pro	Asp 80	
Phe	Asn	Gln	Glu	Ala 85	Tyr	Val	Gly	Gly	Thr 90	Met	Val	Arg	Ser	Gly 95	Gln	
Asp	Pro	Tyr	Ala 100	Arg	Asn	Lys	Phe	Asn 105	Gln	Val	Glu	Ser	Asp 110	Lys	Leu	
Arg	Met	Asp 115	Arg	Ala	Ile	Pro	Asp 120	Thr	Arg	His	Asp	Gln 125	Cys	Gln	Arg	
Lys	Gln 130	Trp	Arg	Val	Asp	Leu 135	Pro	Ala	Thr	Ser	Val 140	Val	Ile	Thr	Phe	
His 145	Asn	Glu	Ala	Arg	Ser 150	Ala	Leu	Leu	Arg	Thr 155	Val	Val	Ser	Val	Leu 160	
Lys	Lys	Ser	Pro	Pro 165	His	Leu	Ile	Lys	Glu 170	Ile	Ile	Leu	Val	Asp 175	Asp	
Tyr	Ser	Asn	Asp 180	Pro	Glu	Asp	Gly	Ala 185	Leu	Leu	Gly	Lys	Ile 190	Glu	Lys	
Val	Arg	Val 195	Leu	Arg	Asn	Asp	Arg 200	Arg	Glu	Gly	Leu	Met 205	Arg	Ser	Arg	
Val	Arg 210	Gly	Ala	Asp	Ala	Ala 215	Gln	Ala	Lys	Val	Leu 220	Thr	Phe	Leu	Asp	
Ser 225	His	Cys	Glu	Cys	Asn 230	Glu	His	Trp	Leu	Glu 235	Pro	Leu	Leu	Glu	Arg 240	
Val	Ala	Glu	Asp	Arg 245	Thr	Arg	Val	Val	Ser 250	Pro	Ile	Ile	Asp	Val 255	Ile	
Asn	Met	Asp	Asn 260	Phe	Gln	Tyr	Val	Gly 265	Ala	Ser	Ala	Asp	Leu 270	Lys	Gly	
Gly	Phe	Asp 275	Trp	Asn	Leu	Val	Phe 280	Lys	Trp	Asp	Tyr	Met 285	Thr	Pro	Glu	

FIG. 13A

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Gln	Arg	Arg	Ser	Arg	Gln	Gly	Asn	Pro	Val	Ala	Pro	Ile	Lys	Thr	Pro
290						295					300				
Met	Ile	Ala	Gly	Gly	Leu	Phe	Val	Met	Asp	Lys	Phe	Tyr	Phe	Glu	Glu
305					310					315					320
Leu	Gly	Lys	Tyr	Asp	Met	Met	Met	Asp	Val	Trp	Gly	Gly	Glu	Asn	Leu
				325					330					335	
Glu	Ile	Ser	Phe	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Leu	Glu	Ile	Ile
			340					345					350		
Pro	Cys	Ser	Arg	Val	Gly	His	Val	Phe	Arg	Lys	Gln	His	Pro	Tyr	Thr
		355					360					365			
Phe	Pro	Gly	Gly	Ser	Gly	Thr	Val	Phe	Ala	Arg	Asn	Thr	Arg	Arg	Ala
	370					375					380				
Ala	Glu	Val	Trp	Met	Asp	Glu	Tyr	Lys	Asn	Phe	Tyr	Tyr	Ala	Ala	Val
385					390					395					400
Pro	Ser	Ala	Arg	Asn	Val	Pro	Tyr	Gly	Asn	Ile	Gln	Ser	Arg	Leu	Glu
				405					410					415	
Leu	Arg	Lys	Lys	Leu	Ser	Cys	Lys	Pro	Phe	Lys	Trp	Tyr	Leu	Glu	Asn
			420					425					430		
Val	Tyr	Pro	Glu	Leu	Arg	Val	Pro	Asp	His	Gln	Asp	Ile	Ala	Phe	Gly
		435					440					445			
Ala	Leu	Gln	Gln	Gly	Thr	Asn	Cys	Leu	Asp	Thr	Leu	Gly	His	Phe	Ala
	450					455					460				
Asp	Gly	Val	Val	Gly	Val	Tyr	Glu	Cys	His	Asn	Ala	Gly	Gly	Asn	Gln
465					470					475					480
Glu	Trp	Ala	Leu	Thr	Lys	Glu	Lys	Ser	Val	Lys	His	Met	Asp	Leu	Cys
				485					490					495	
Leu	Thr	Val	Val	Asp	Arg	Ala	Pro	Gly	Ser	Leu	Ile	Lys	Leu	Gln	Gly
			500					505					510		
Cys	Arg	Glu	Asn	Asp	Ser	Arg	Gln	Lys	Trp	Glu	Gln	Ile	Glu	Gly	Asn
		515					520					525			
Ser	Lys	Leu	Arg	His	Val	Gly	Ser	Asn	Leu	Cys	Leu	Asp	Ser	Arg	Thr
	530					535					540				
Ala	Lys	Ser	Gly	Gly	Leu	Ser	Val	Glu	Val	Cys	Gly	Pro	Ala	Leu	Ser
545					550					555					560
Gln	Gln	Trp	Lys	Phe	Thr	Leu	Asn	Leu	Gln	Gln					
				565					570						

FIG. 13A (CONT.)
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Nucleic acid sequence

atgagggggc	gctogoggat	gctgctctgc	ttogocttcc	tgtgggtgct	gggcattogcc	60
tactacatgt	actcgggggg	cggctctgog	ctggccgggg	gagcgggggg	cggcggcggc	120
aggaaggagg	actggaatga	aattgacccc	attaaaaaga	aagaccttca	tcacagcaat	180
ggagaagaga	aagcacaag	catggagacc	ctccctccag	ggaaagtacg	gtggccagac	240
tttaaccagg	aagcttatgt	tggagggaog	atggctccgt	cggggcagga	cccttaacgc	300
cgcaacaagt	tcaaccagg	ggagagtgat	aagcttogaa	tggacagagc	catccctgac	360
acccggcatg	accagtgta	goggaagcag	tggcgggtgg	atctgcgggc	caaccaggtg	420
gtgatcacgt	ttcacaatga	agccaggctg	gcccactcca	ggacogtggt	cagcgtgctt	480
aagaaaagcc	cgcgccatct	cataaaaaga	atcatcttgg	tggatgacta	cagcaatgat	540
octgaggagc	gggctctctt	ggggaaaatt	gagaaagtgc	gagttcttag	aaatgatoga	600
cgaagaaggcc	tcattgogctc	acgggttogg	ggggccgatg	ctgcaccaagc	caaggctcgt	660
accttctcgg	acagtcactg	cgagtgtaat	gagcactggc	tggagccct	octggaaaagg	720
gtggcggagg	acaggactcg	ggttgtgtca	cccatcatcg	atgtcattaa	tatggacaac	780
tttcagtatg	tgggggcac	tgctgacttg	aaggcggggt	ttgattggaa	cttgggtattc	840
aagtgggatt	acattgagcc	tgagcagaga	aggtcccgcc	aggggaaccc	agtcgcccct	900
ataaaaaacc	ccattgattgc	tgggtgggctg	tttgtgatgg	ataagttcta	ttttgaagaa	960
ctgggggaagt	acgacatgat	gatggatgtg	tggggaggag	agaacctaga	gatctcgttc	1020
cgggtgtggc	agtggtgtgg	cagcctggag	atcatcccg	gcagccgtgt	gggacacgtg	1080
ttccggagc	agcaccocca	ccggttcccg	ggtggcagtg	gcactgtctt	tgcocgaaac	1140
acccgcgggg	cagcagaggt	ctggatggat	gaatacaaaa	atttctatta	tgcagcagtg	1200
octtctgcta	gaaacgttcc	ttatggaaat	attcagagca	gattggagct	taggaagaaa	1260
ctcagctgca	agoccttcca	atggtaoctt	gaaaatgtct	atocagagtt	aagggttcca	1320
gaccatcagg	atatagcttt	tggggccttg	cagcagggaa	ctaactgct	cgacactttg	1380
ggacactttg	ctgatgtgtg	ggttggagtt	tatgaatgtc	acaatgctgg	gggaaaccag	1440
gaatgggct	tgacgaagga	gaagtogggt	aagcaccatg	atttgtgct	tactgtgggtg	1500
gacggggcac	cgggctctct	tataaagctg	cagggctgoc	gagaaaatga	cagcagacag	1560
aaatgggaac	agatcgaggg	caactccaag	ctgaggcagc	tgggcagcaa	octgtgctcg	1620
gacagtogca	cggccaagag	cgggggccta	agcgtggagg	tgtgtggccc	ggccctttcg	1680
cagcagtgga	agttcacgct	caacctgcag	cag			1713

FIG. 13B
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**Δ51 UDP-N-acetylgalactosaminyltransferase 2, GalNAcT2,
nucleic acid and amino acid sequences**

Amino acid sequence

Lys	Lys	Lys	Asp	Leu	His	His	Ser	Asn	Gly	Glu	Glu	Lys	Ala	Gln	Ser	1	5	10	15
Met	Glu	Thr	Leu	Pro	Pro	Gly	Lys	Val	Arg	Trp	Pro	Asp	Phe	Asn	Gln	20	25	30	
Glu	Ala	Tyr	Val	Gly	Gly	Thr	Met	Val	Arg	Ser	Gly	Gln	Asp	Pro	Tyr	35	40	45	
Ala	Arg	Asn	Lys	Phe	Asn	Gln	Val	Glu	Ser	Asp	Lys	Leu	Arg	Met	Asp	50	55	60	
Arg	Ala	Ile	Pro	Asp	Thr	Arg	His	Asp	Gln	Cys	Gln	Arg	Lys	Gln	Trp	65	70	75	80
Arg	Val	Asp	Leu	Pro	Ala	Thr	Ser	Val	Val	Ile	Thr	Phe	His	Asn	Glu	85	90	95	
Ala	Arg	Ser	Ala	Leu	Leu	Arg	Thr	Val	Val	Ser	Val	Leu	Lys	Lys	Ser	100	105	110	
Pro	Pro	His	Leu	Ile	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Tyr	Ser	Asn	115	120	125	
Asp	Pro	Glu	Asp	Gly	Ala	Leu	Leu	Gly	Lys	Ile	Glu	Lys	Val	Arg	Val	130	135	140	
Leu	Arg	Asn	Asp	Arg	Arg	Glu	Gly	Leu	Met	Arg	Ser	Arg	Val	Arg	Gly	145	150	155	160
Ala	Asp	Ala	Ala	Gln	Ala	Lys	Val	Leu	Thr	Phe	Leu	Asp	Ser	His	Cys	165	170	175	
Glu	Cys	Asn	Glu	His	Trp	Leu	Glu	Pro	Leu	Leu	Glu	Arg	Val	Ala	Glu	180	185	190	
Asp	Arg	Thr	Arg	Val	Val	Ser	Pro	Ile	Ile	Asp	Val	Ile	Asn	Met	Asp	195	200	205	
Asn	Phe	Gln	Tyr	Val	Gly	Ala	Ser	Ala	Asp	Leu	Lys	Gly	Gly	Phe	Asp	210	215	220	
Trp	Asn	Leu	Val	Phe	Lys	Trp	Asp	Tyr	Met	Thr	Pro	Glu	Gln	Arg	Arg	225	230	235	240
Ser	Arg	Gln	Gly	Asn	Pro	Val	Ala	Pro	Ile	Lys	Thr	Pro	Met	Ile	Ala	245	250	255	
Gly	Gly	Leu	Phe	Val	Met	Asp	Lys	Phe	Tyr	Phe	Glu	Glu	Leu	Gly	Lys	260	265	270	
Tyr	Asp	Met	Met	Met	Asp	Val	Trp	Gly	Gly	Glu	Asn	Leu	Glu	Ile	Ser	275	280	285	
Phe	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Leu	Glu	Ile	Ile	Pro	Cys	Ser				

FIG. 14A
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290		295		300											
Arg 305	Val	Gly	His	Val	Phe 310	Arg	Lys	Gln	His	Pro 315	Tyr	Thr	Phe	Pro	Gly 320
Gly	Ser	Gly	Thr	Val 325	Phe	Ala	Arg	Asn	Thr 330	Arg	Arg	Ala	Ala	Glu 335	Val
Trp	Met	Asp	Glu 340	Tyr	Lys	Asn	Phe	Tyr 345	Tyr	Ala	Ala	Val	Pro 350	Ser	Ala
Arg	Asn	Val 355	Pro	Tyr	Gly	Asn	Ile 360	Gln	Ser	Arg	Leu	Glu 365	Leu	Arg	Lys
Lys	Leu 370	Ser	Cys	Lys	Pro	Phe 375	Lys	Trp	Tyr	Leu	Glu 380	Asn	Val	Tyr	Pro
Glu 385	Leu	Arg	Val	Pro	Asp 390	His	Gln	Asp	Ile	Ala 395	Phe	Gly	Ala	Leu	Gln 400
Gln	Gly	Thr	Asn	Cys 405	Leu	Asp	Thr	Leu	Gly 410	His	Phe	Ala	Asp	Gly 415	Val
Val	Gly	Val	Tyr 420	Glu	Cys	His	Asn	Ala 425	Gly	Gly	Asn	Gln	Glu 430	Trp	Ala
Leu	Thr	Lys 435	Glu	Lys	Ser	Val	Lys 440	His	Met	Asp	Leu	Cys 445	Leu	Thr	Val
Val	Asp 450	Arg	Ala	Pro	Gly	Ser 455	Leu	Ile	Lys	Leu	Gln 460	Gly	Cys	Arg	Glu
Asn 465	Asp	Ser	Arg	Gln	Lys 470	Trp	Glu	Gln	Ile	Glu 475	Gly	Asn	Ser	Lys	Leu 480
Arg	His	Val	Gly	Ser 485	Asn	Leu	Cys	Leu	Asp 490	Ser	Arg	Thr	Ala	Lys 495	Ser
Gly	Gly	Leu	Ser 500	Val	Glu	Val	Cys	Gly 505	Pro	Ala	Leu	Ser	Gln 510	Gln	Trp
Lys	Phe	Thr 515	Leu	Asn	Leu	Gln 520	Gln								

FIG. 14A (CONT.)

Nucleic acid sequence	18/54	
aaaaagaaag aoccttcatca cagcaatgga gaagagaaag cacaagcat ggagaoctc		60
octocagggg aagtacgggtg gacagacttt aaccaggaag cttatgttgg agggacgatg		120
gtccgctcgg ggcaggaccc ttacgcccgc aacaagttca accaggtgga gagtgataag		180
cttogaatgg acagagccat cctgacacc cggcatgacc agtgtcagcg gaagcagtg		240
cggttgatc tgccggccac cagcgtgggtg atcaagtttc acaatgaagc caggtcggcc		300
ctactcagga ccgtggtcag cgtgcttaag aaaagcccgc cccatctcat aaaagaaatc		360
atcttggtgg atgactacag caatgatcct gaggaacggg cttctcttgg gaaaattgag		420
aaagtgcgag ttcttagaaa tgatogaaga gaaggcctca tgccgtcagg ggttcggggg		480
gocgatgctg cccaagccaa ggtcctgacc ttctggaca gtcactgaga gtgtaattgag		540
cactggctgg agccctcct ggaaaggggtg gcggaggaca ggactcgggt tgtgtcaacc		600
atcatogatg tcattaatat ggacaacttt cagtatgtgg ggccatctgc tgacttgaag		660
ggcggttttg attggaactt ggtattcaag tgggattaca tgacgctga gcagagaagg		720
tcocggcagg ggaaccagc cgcacctata aaaaccccca tgattgctgg tgggctgttt		780
gtgatggata agttctatct tgaagaactg ggaagtaag acatgatgat ggatgtgtgg		840
ggaggagaga aactagagat ctogtccgc gtgtggcagt gtgggtggcag cctggagatc		900
atcccgtaga gcgtgtggg acacgtgttc cggagcagc accctacac gttccgggt		960
ggcagtggca ctgtctttgc ccgaacacc cgcggggcag cagaggtctg gatggatgaa		1020
tacaaaaatt tctattatgc agcagtgcct tctgctagaa acgttctta tggaaatatt		1080
cagagcagat tggagcttag gaagaaactc agctgcaagc cttcaaagt gtacctgaa		1140
aatgtctatc cagagttaag ggttcagac catcaggata tagcttttgg ggcttgacg		1200
cagggaacta actgcctaga cactttggga cactttgctg atggtgtggt tggagtatat		1260
gaatgtcaca atgctgggg aaaccaggaa tgggcttga cgaaggagaa gtccgtgaag		1320
cacatggatt tgtgccttac tgtggtggac cgggcaacgg gctctcttat aaagctgcag		1380
ggctgcagag aaaatgacag cagacagaaa tgggaacaga togagggcaa ctccaagctg		1440
aggcaogtgg gcagcaact gtgcctggac agtgcacgg ccaagagcgg gggttaagc		1500
gtggaggtgt gtggccggc cctttgcag cagtggaggt tcaogctcaa octgcagcag		1560

FIG. 14B

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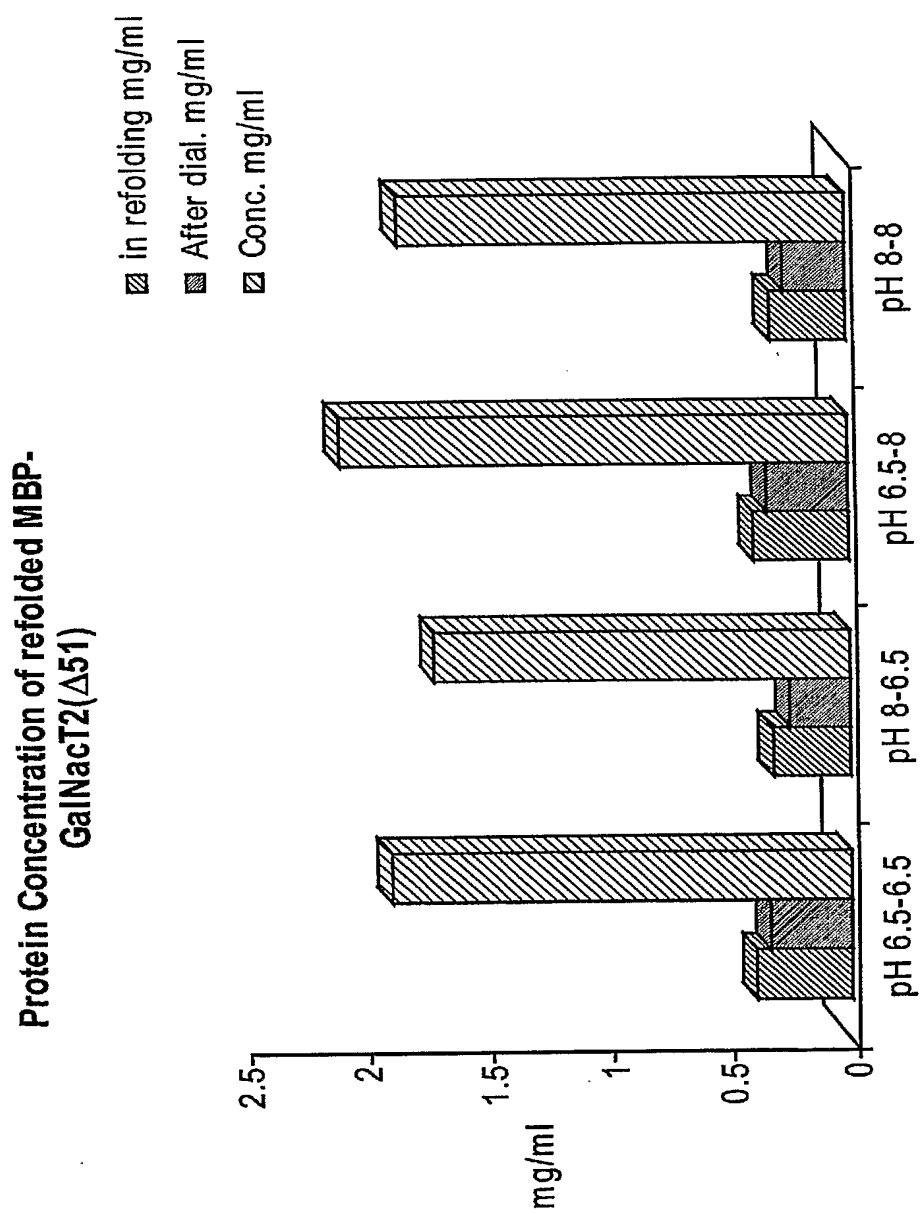


FIG. 15

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GaINAct2 activities of refolded MBP-
GaINAct2(D51)

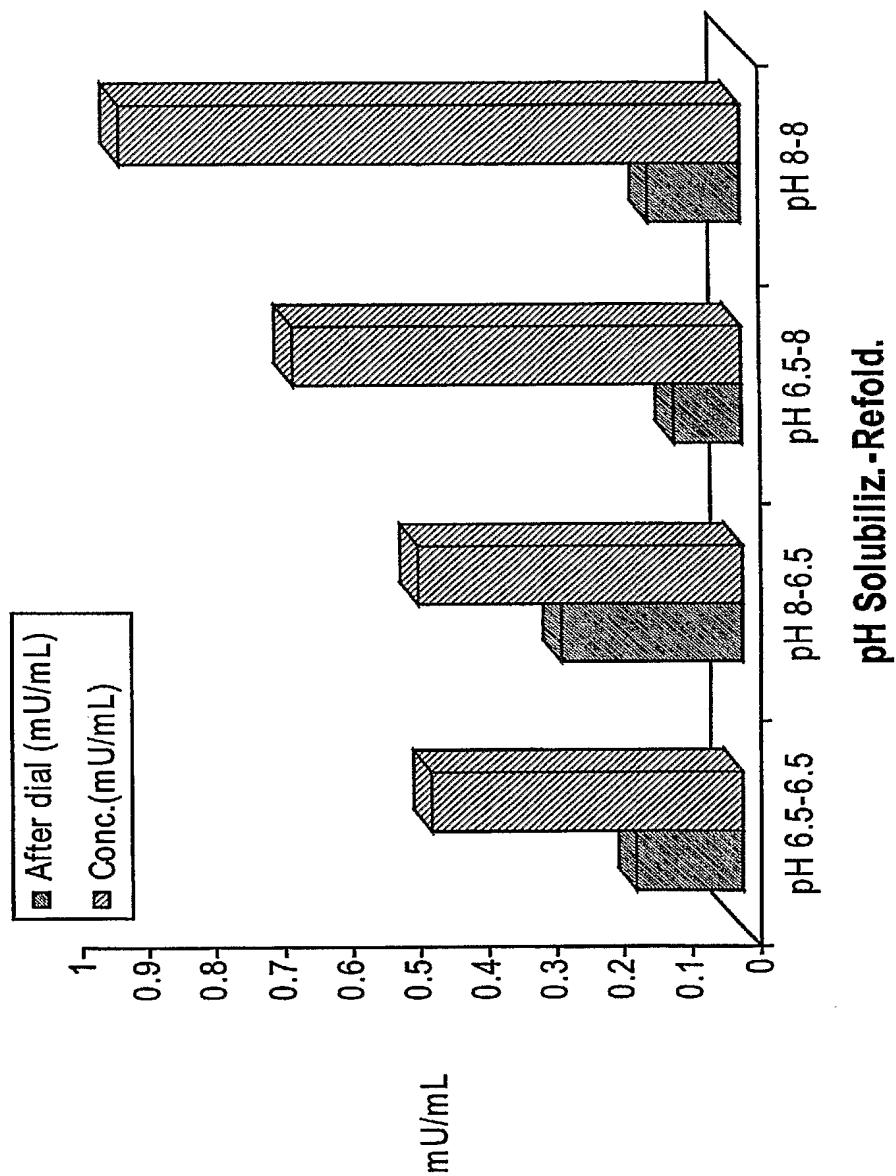


FIG. 16

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pH effect on the MBP-GalNAcT2(D51) specific activities

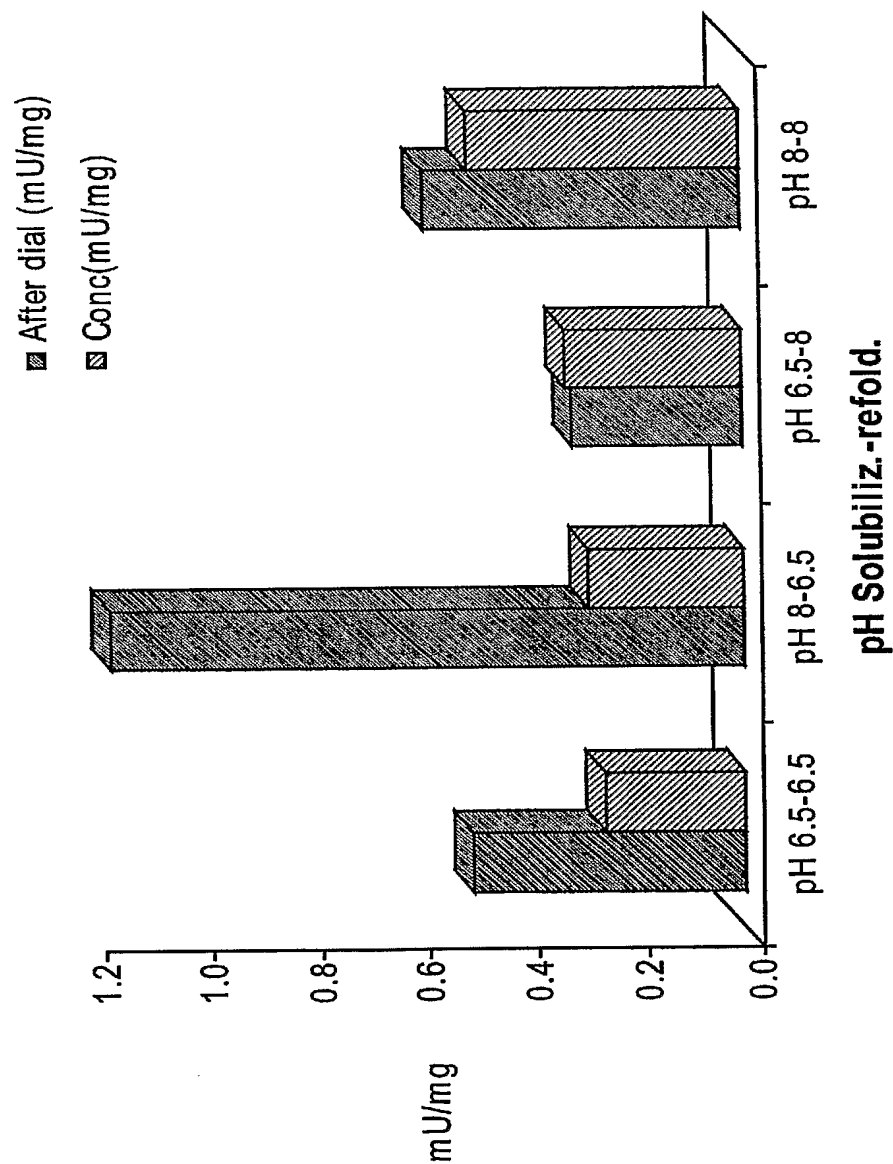


FIG. 17

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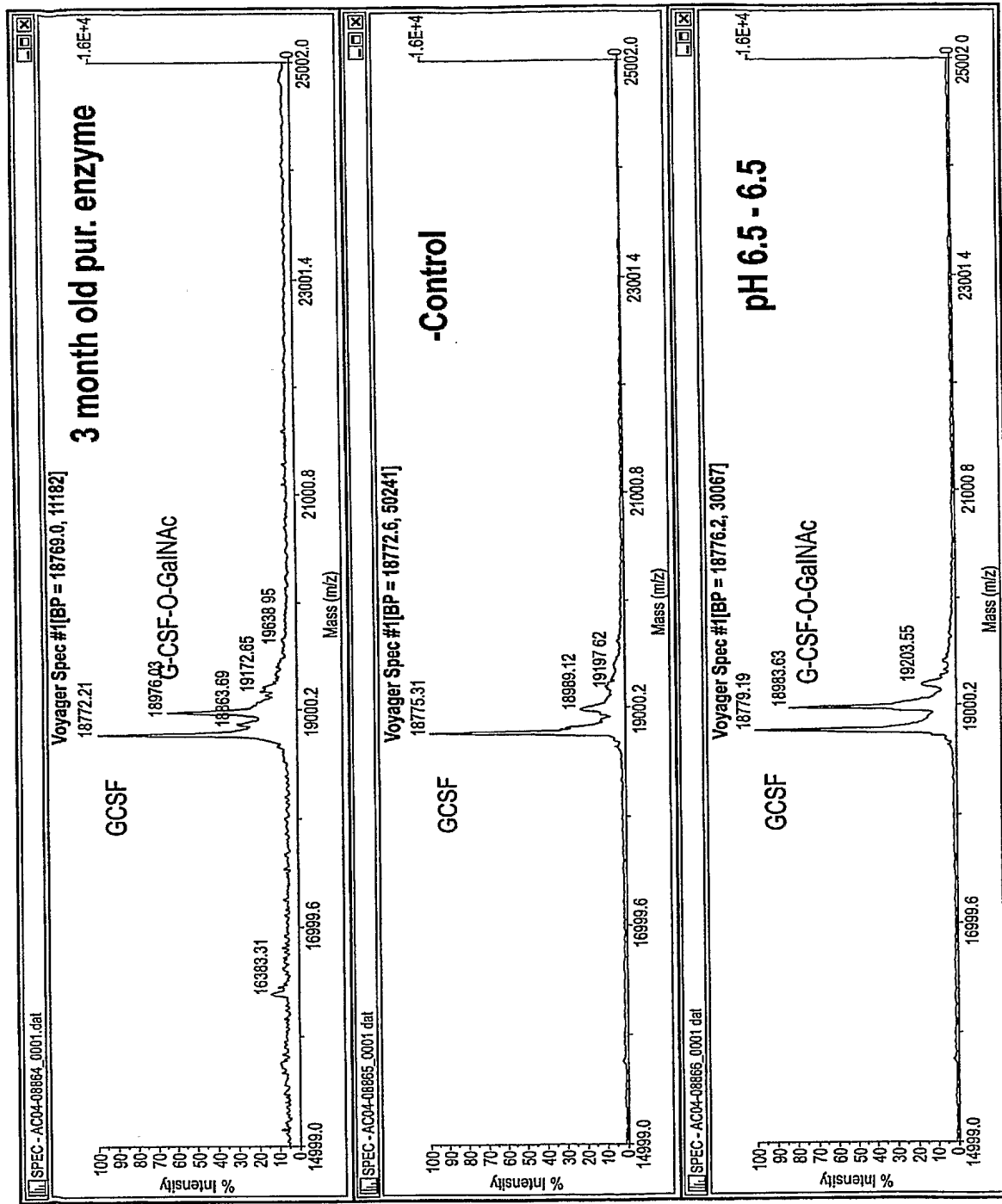


FIG. 18A

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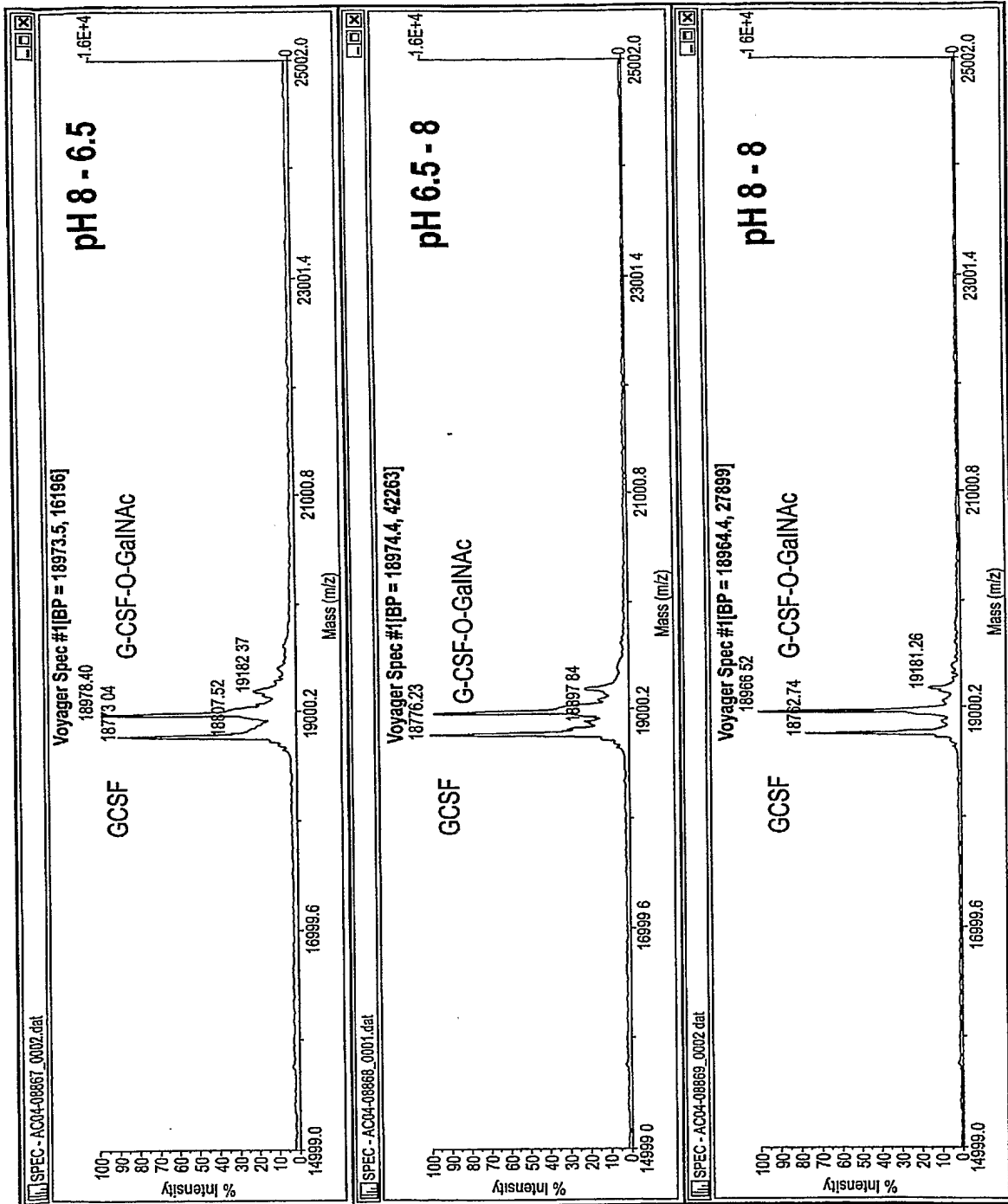


FIG. 18B

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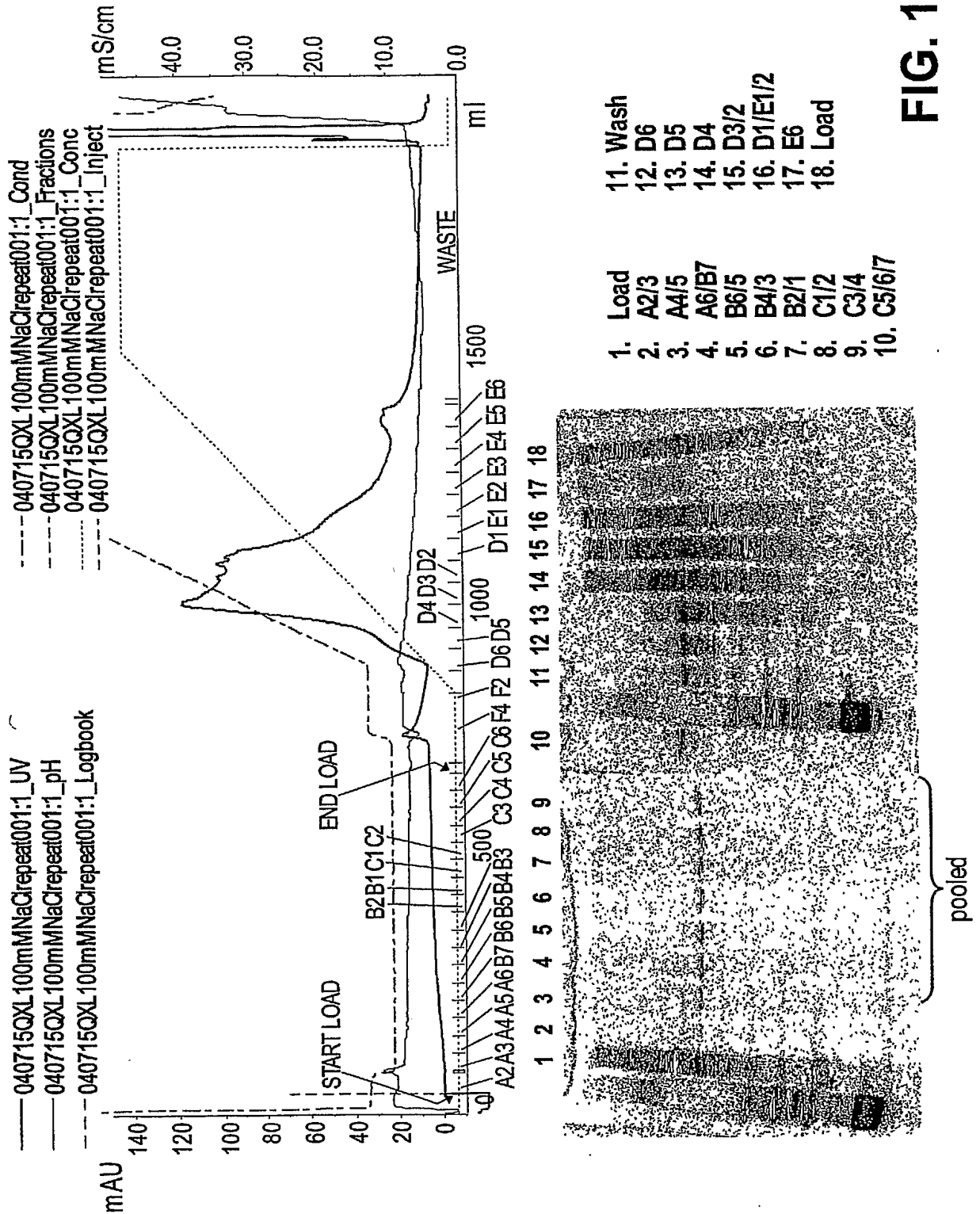


FIG. 19

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	Volume (mL)	Activity (U/L)	A280
Load	890	1.5	0.110
FT _{A4-C4}	670	9.2	NA
FT _{C5-C7}	120	1.0	0
Wash	138	3.6	0.100
D6	45	4.5	0
D5	45	2.4	0.026
D4	45	2.0	0.108
D3/2	90	1.1	0.179
E6		0.0	0.017

FIG. 20

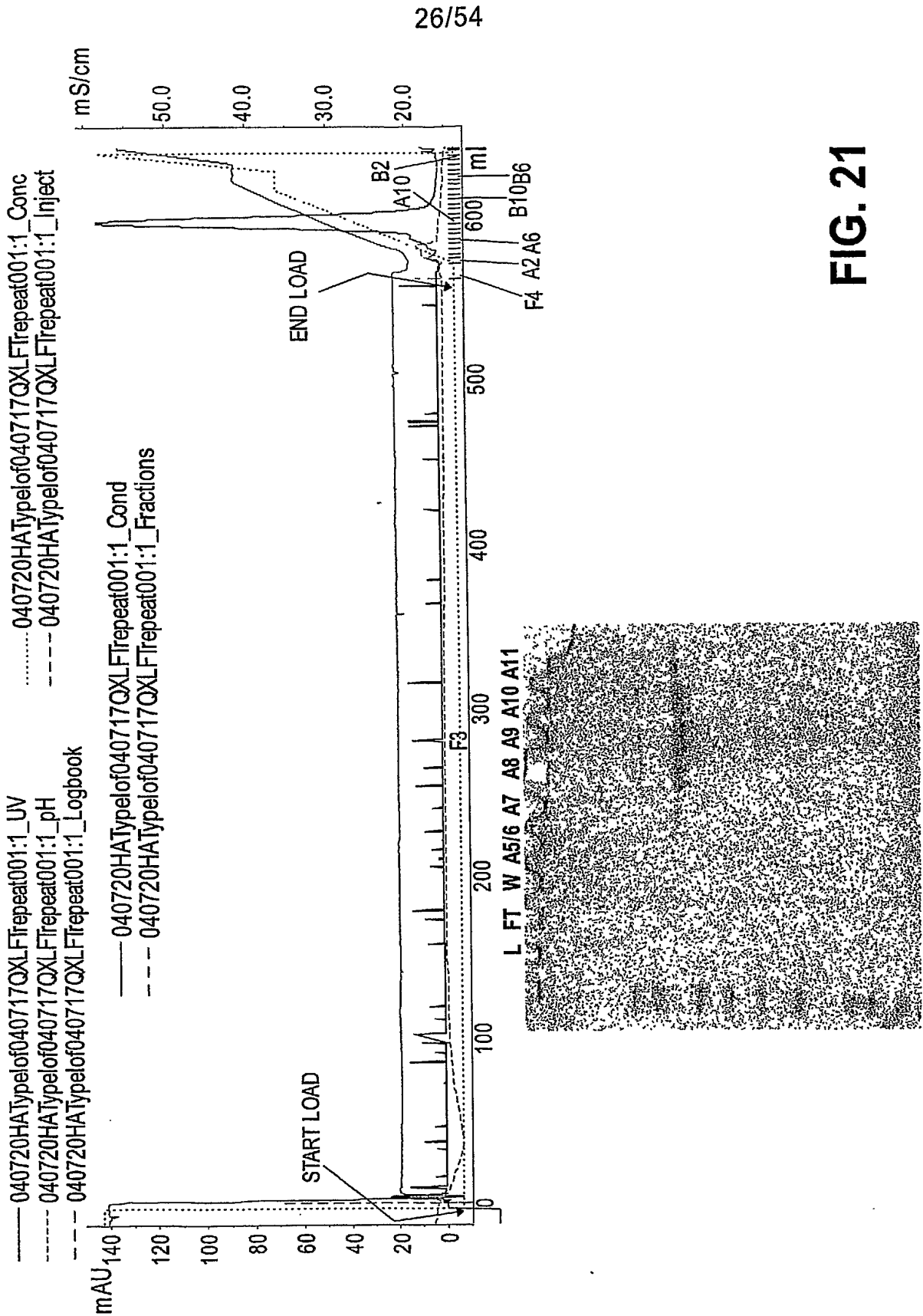


FIG. 21

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Pooled A4-C4 and adjusted pH to 7.0 using 1mM HCl 670mL
load pH 7.0 16mS/cm

	Volume (mL)	Activity (U/L) pre- dialysis	Activity (U/L) post- dialysis	A280	A280/ 1.51 (mg/mL)	Activity (U)	Mass (mg)	Specific Activity (U/mg)
Load	670	9.2	NA	NA				
FT	670	0.0	NA	0.122				
Wash	9	2.9	NA	-0.013				
A5/6	6	1.1	NA	-0.005				
A7	3	0.1	19.3 (13mL)	0.180	0.119	0.25	1.55	0.16
A8	3	1.3						
A9	3	4.6						
A10	3	2.4						
A11	3	0.4						

FIG. 22

COMPARISON of MBP with MBP-SBD₃₉ tag in ST3Gal3 in Cyclodextrin column purification

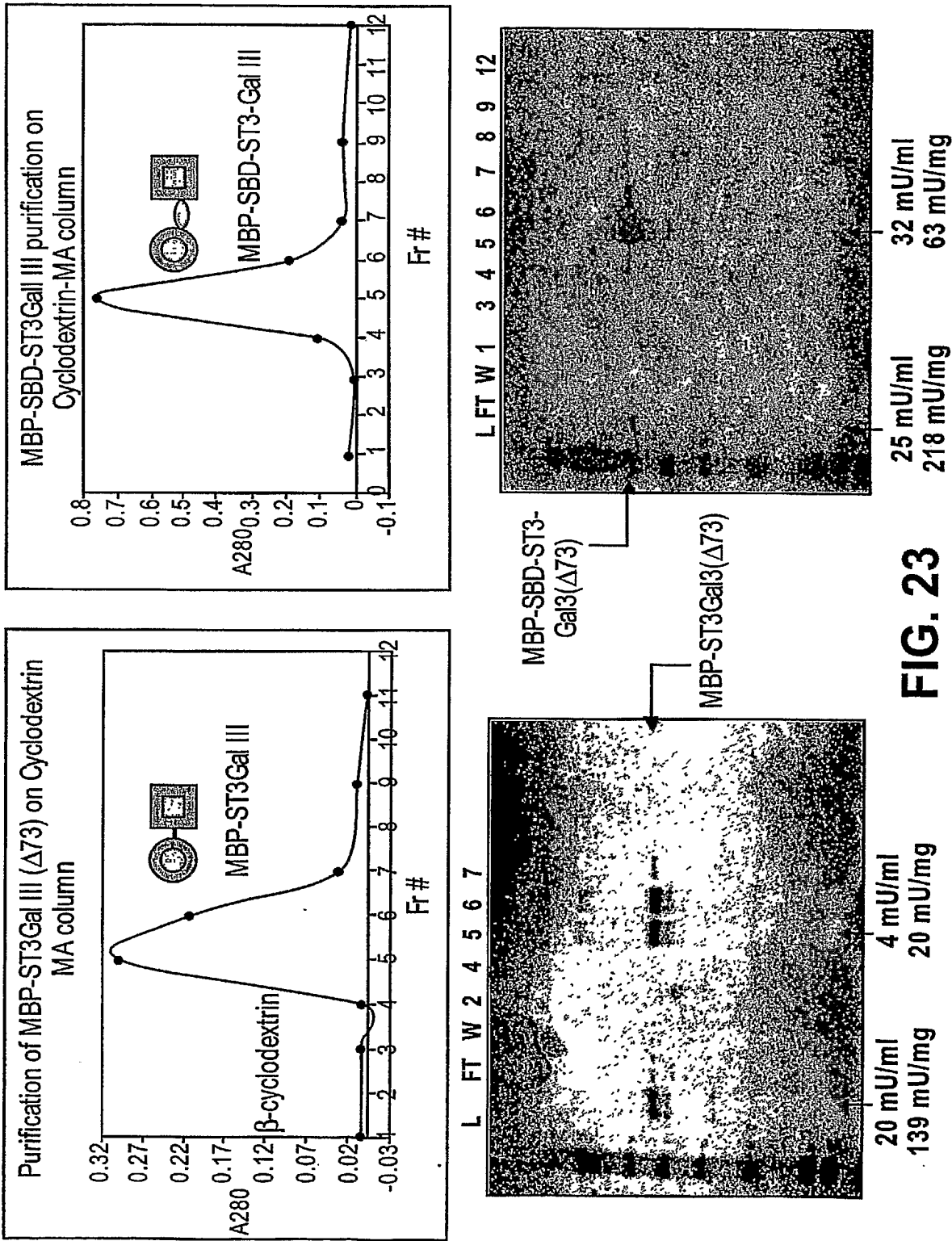


FIG. 23

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MBP-pST3Gal1 fusion protein

MKIEGKLVINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIFWAHDF
 GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALD
 KELKAKGKSALMFNLQEPYFTWPLIADGGYAFKYENGKYDIKDVGVNDAGAKAGLFLVDLIKNGH
 MNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTPLPTFKGQPSKPFVGLSAGINAASP
 NKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIQMSAF
 WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNLIEGRISEFGSELSSEFKKLMKYPYR
 PCTCTRCIEEQRVSAWDERFNRSMQPLLTAKNAHLEEDTYKWWLRQREKQPNNLNDTRELQVVP
 GNVDPILLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHFVYPE
 SFRELAQEVSMILVPFKTTDLEWVISATTTGRISHTYVVPVPAKIKVKKKELIYHPAFIKYVFDRWLQGH
 GRYPSTGILSVIFSLHICDEVLDYGFADSKGNWHHYWENNPSAGAFRKTGVHDGDFESNVTTILASIN
 KIRIFKGR

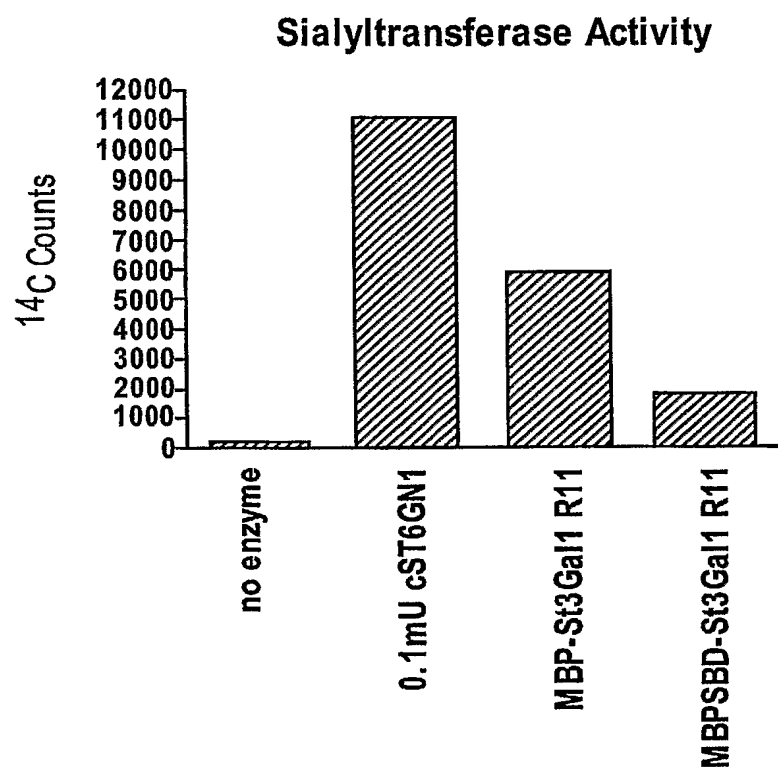
FIG. 24A

MBPSBD-pST3Gal1 fusion protein

MKIEGKLVINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIFWAHDF
 GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALD
 KELKAKGKSALMFNLQEPYFTWPLIADGGYAFKYENGKYDIKDVGVNDAGAKAGLFLVDLIKNGH
 MNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTPLPTFKGQPSKPFVGLSAGINAASP
 NKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIQMSAF
 WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNLIEGRISEFGSIVATGGTTTATPTG
 SGSVTSTSKTTATASKTSTSTSTSTCTPTAVAVTFDLTATTYGENIYLVGSISQLGDWETSDGIALSAD
 KYTSSDPLWYVTVTLPAGESEYKFFRIESDDSVESDPNREYTVPQACGTSTATVTDTWRGSELSEN
 FKLMKYPYRPCTCTRCIEEQRVSAWDERFNRSMQPLLTAKNAHLEEDTYKWWLRQREKQPNNLN
 DTIRELFQVVPGNVDPLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADV
 SKTTHHFVYPESFRELAQEVSMILVPFKTTDLEWVISATTTGRISHTYVVPVPAKIKVKKKELIYHPAFIK
 YVFDRWLQGHGRYPSTGILSVIFSLHICDEVLDYGFADSKGNWHHYWENNPSAGAFRKTGVHDGDF
 ESNVTTILASINKIRIFKGR

FIG. 24B

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Test pST3Gal1 for activity after Hampton refold

FIG. 25

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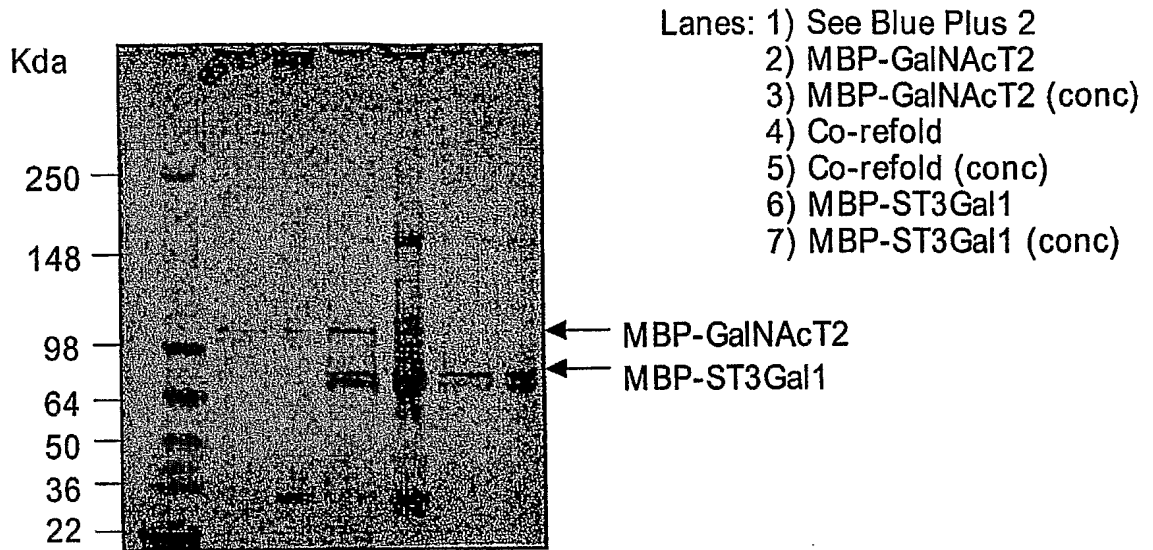
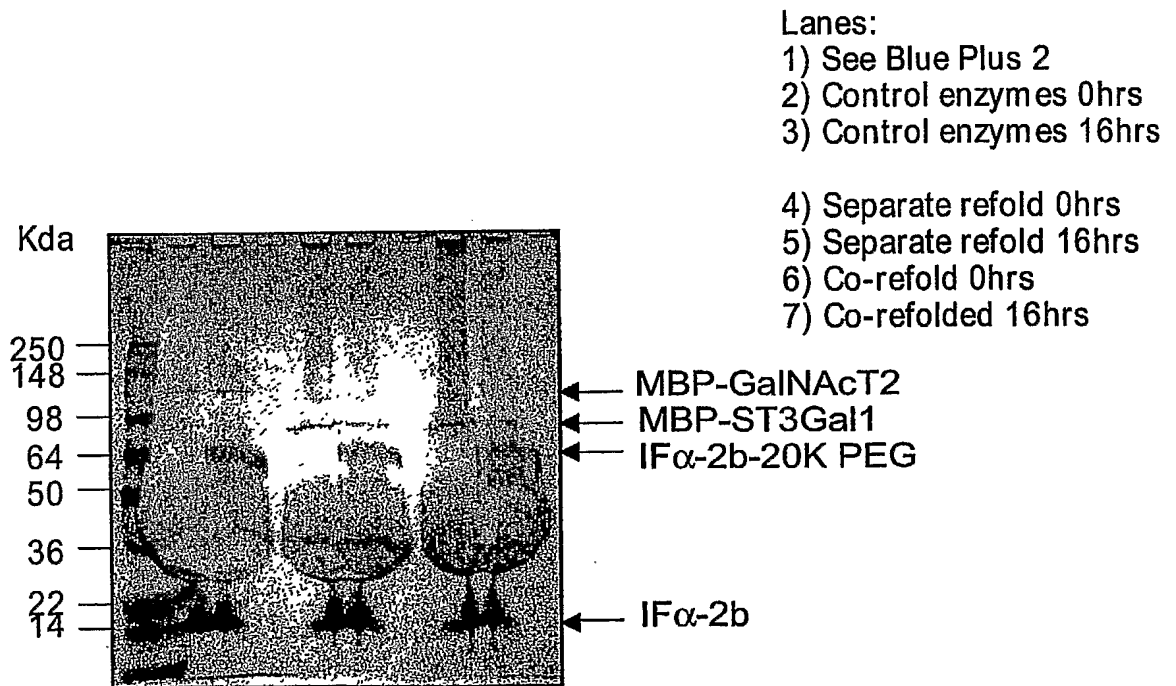
MKIEGKLVWINGDKGYNGLAEVGKKFEKDTGKVTVEHPDKLEEKFPQVAATGDGPDIFWAHDRF
 GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLYNNKDLLPNPPKTWEEIPALD
 KELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDKIDVGVNDAGAKAGLFLVDLIKXKH
 MNADTDYSIAEAAFNKGETAMTINGFWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGLSAGINAASP
 NKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAF
 WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNLIEGRISEFGSEHLLDKVPRITPGAL
 STRKTPMATGAVPAKKVVQATKSPASSPHPTTRRRQRRLKASEFKSEPRWDEEEYSLDMSSLQT
 NCSASVKKIKASKSPWLQNFELPNITLFLDSGRFTQSEWNRLEHFAFPFGFMELNQSLSVQKVVTFRFP
 PVRQQLLLASLPTGYSKCITCAVVGNGGILNDSRVGREIDSHDYVFRLSGAVIKGYEQDVGTRT
 SFYGFATFSLTQSILILGRRGFQHVPLGKDVRYLHFLGTRNRYEWLEAMFELNQTLAKTHLSWFR
 HRPQEAFRNALDLDRYLLHPDFELRYMKNRFLRSKTLDTAXWRIYRPTTGALLLLTALHLCCKV
 SAYGFITEGHERFSDHYDTSWKRLIFYINHDFLERMVWKRLLHDEGHWLYQRPQSDKAKN

FIG. 26A

MKIEGKLVWINGDKGYNGLAEVGKKFEKDTGKVTVEHPDKLEEKFPQVAATGDGPDIFWAHDRF
 GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLYNNKDLLPNPPKTWEEIPALD
 KELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDKIDVGVNDAGAKAGLFLVDLIKXKH
 MNADTDYSIAEAAFNKGETAMTINGFWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGLSAGINAASP
 NKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAF
 WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNLIEGRISEFGSKEPQTKPSRHQRIE
 NIKERSLQSLAKPKSQAPTRARITTYAEPVPENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDK
 VPHTAQRAAWKSPEKEKTMVNTLSRPGQDAGMASGRTEAQSWSQDTKTTQCGNGGQTRKLTIA
 SRTVSEKHQGAATTAKTLIPKSQHRMLAPTGAVSTRQRKGVTIATVPPKEKKPQATPPAPFQ
 SPTTQRNORLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDS
 RHFNQSEWDRLHFAFPFGFMELNYSLSVQKVVTFRPPVPOQQLLASLPAGSLRCITCAVVNG
 GILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLILGNRGFKNVPLGK
 DVRYLHFLGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHHPDFLRYM
 KNRFRLRSKTLDDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFTEGHERFSDHYDTSWKRLIFY
 INHDFKLEREVWKRLLHDEGHIRLYQRPQGTAKAKN

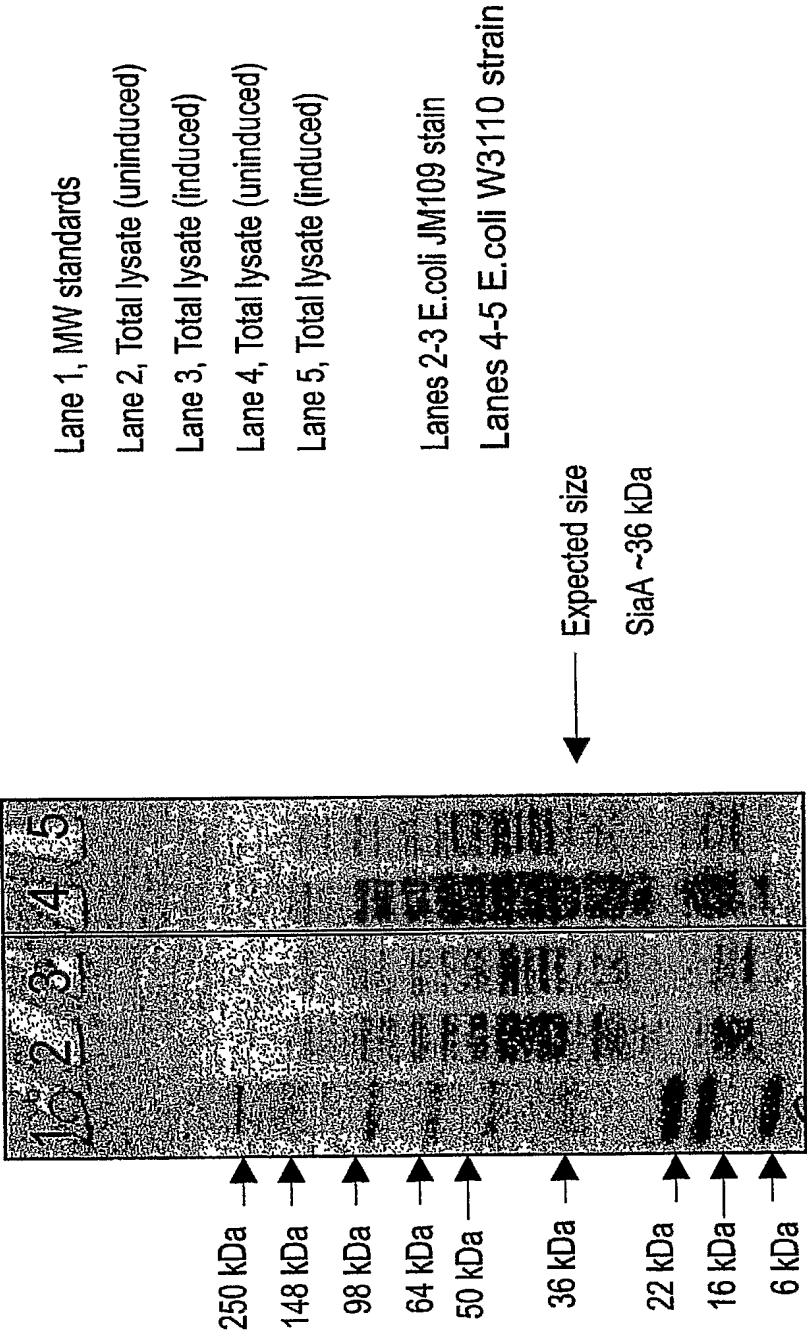
FIG. 26B

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**FIG. 27A****FIG. 27B**

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Induced SiaA expression in E.coli



There is no obvious inducible band at the expected
Mass of 36 kDa for the native SiaA protein.

FIG. 28

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Induced SiaA/MBP expression in E.coli

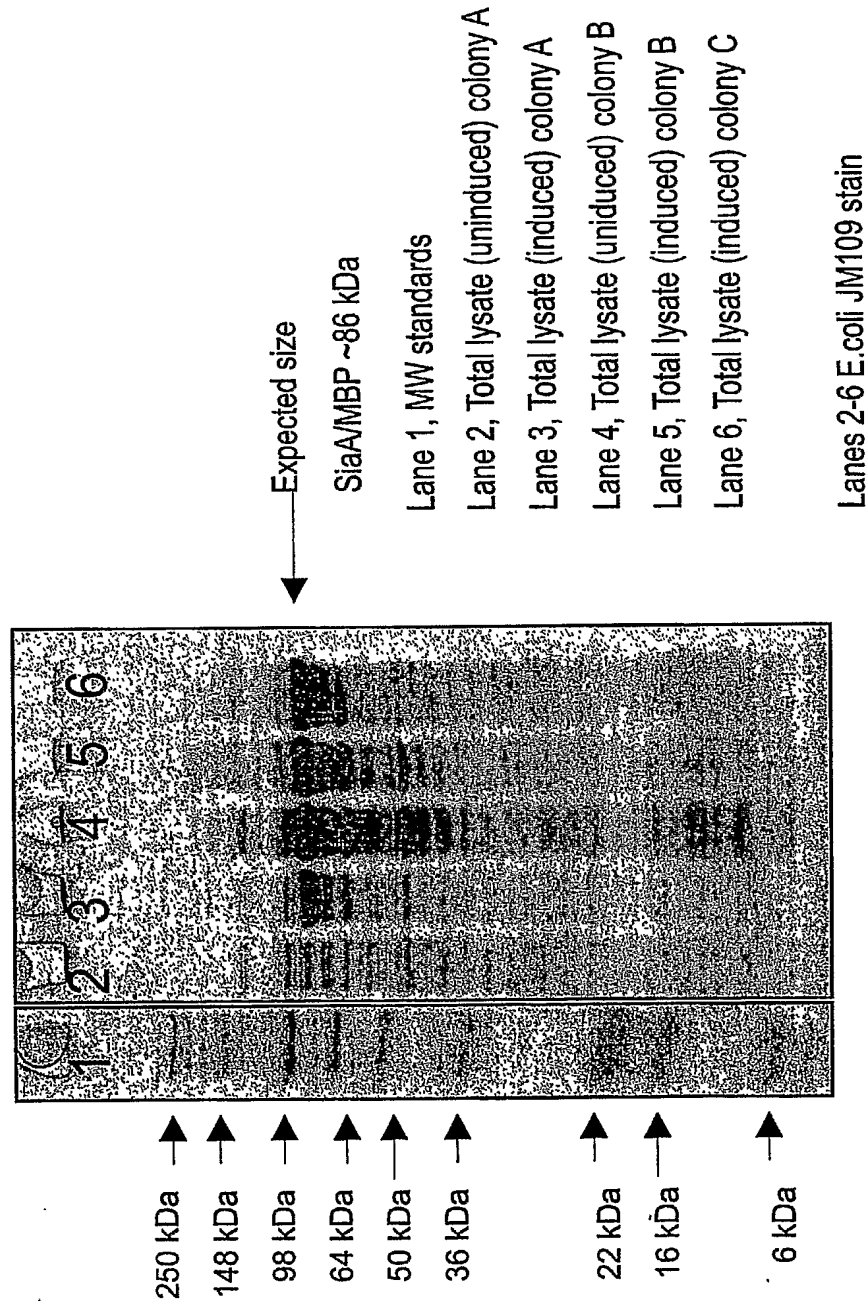


FIG. 29

High level production of SiaA/MBP even in absence of IPTG induction.
Compare to figure X where SiaA production is not obvious. The presence of the fusion partner (MBP) drives high levels of expression.

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```

1  mkfrepllgg saampgaslq racrllvavc alhlgvtlvy ylagrdlrrl pqlvgvhppl
61  qgsshgaaai gqpsgelrlr gvaoppplqn sskprsraps nldayshpgp gpgpgsnlts
121  apvpstttrs ltacpeespl lvgpmliefn ipvdlklieq qnpkvklggr ytpmdcisp
181  kvaiiilfrn rqehlkywly ylhpmvqrqq ldygiyving agesmfnrak llnvgfkeal
241  kdydyncfvf sdvdlipmnd hntyrctfsqp rhisvamdkf gfsipyvqyf ggvsalskqq
301  flsingfpnn ywgwggeddd iynrlafrgm svsrpnavig kcrmihrsd kknepnqrf
361  driahtketm lsdglnsly mvlevqryp1 ytkitvdigt ps

```

FIG. 30

Bovine (b) GalT1 (β 1,4GalT1) constructs

UDP-galactose β -N-acetylglucosaminide β 4-galactosyltransferase (EC 2.4.1.38)

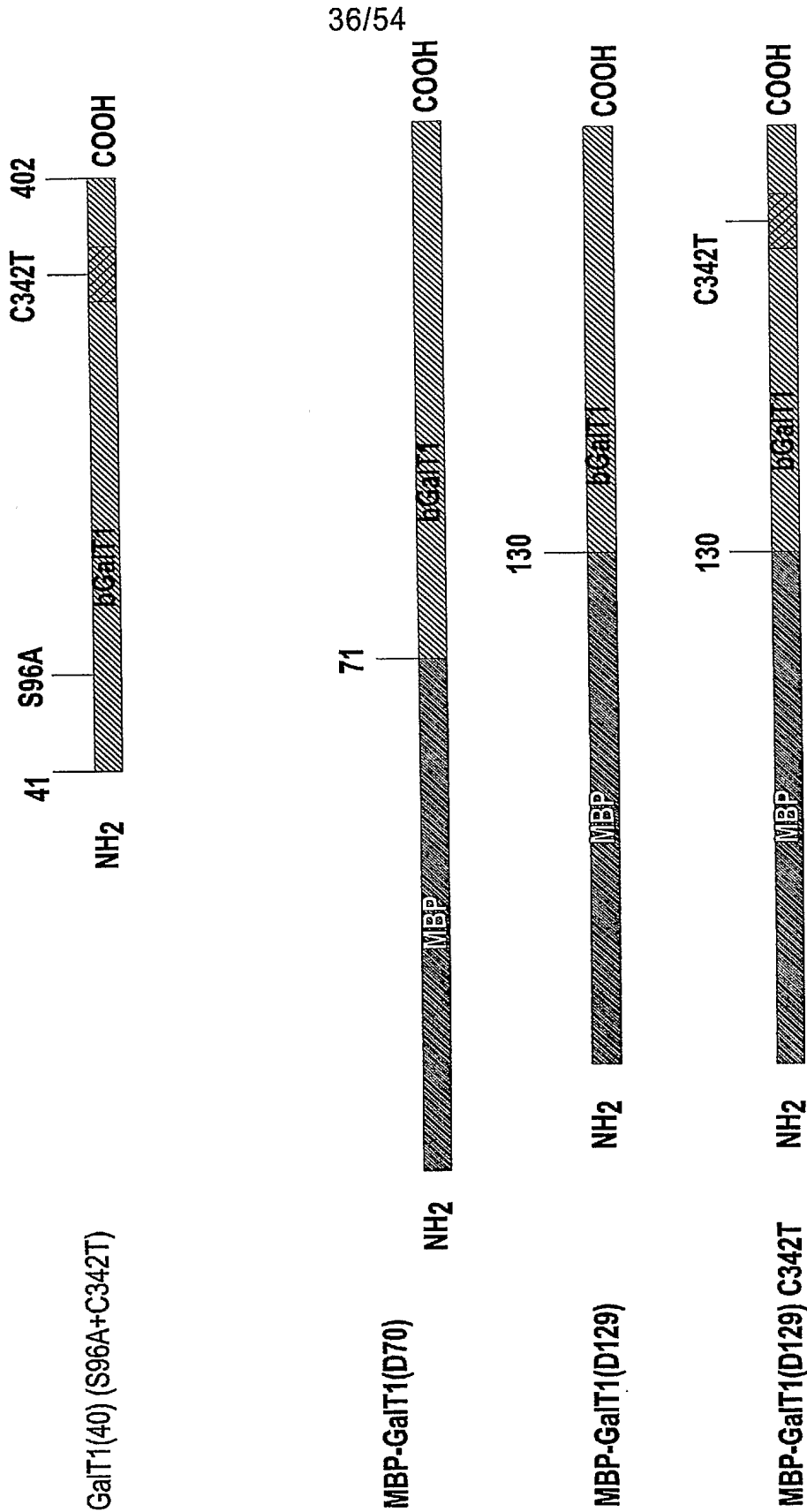
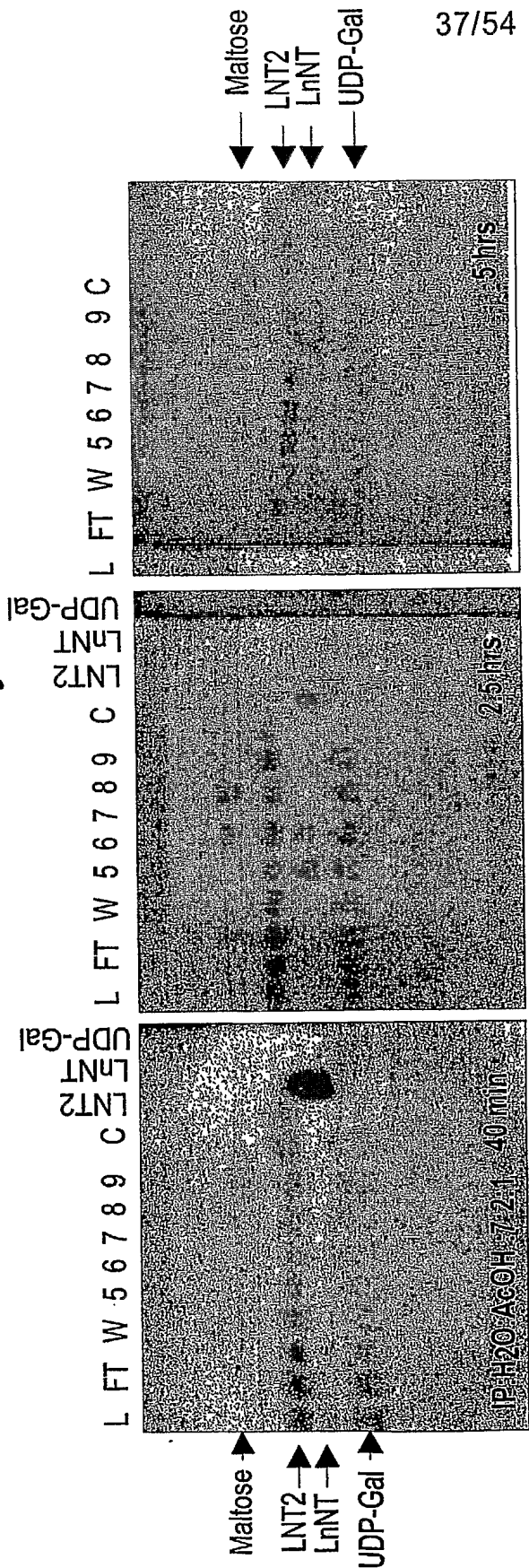


FIG. 31

GalT1 TLC assay



LnNT reactions with

- L: Loaded sample (refolded, dialyzed MBP-GalT1(70) onto amylose column)
- FT: Amylose column Flow trough
- W: Amylose column wash
- 5: Maltose Eluted Fr # 5
- 6: Maltose Eluted Fr # 6
- 7: Maltose Eluted Fr # 7
- 8: Maltose Eluted Fr # 8
- 9: Maltose Eluted Fr # 9
- C: Control with water

FIG. 32

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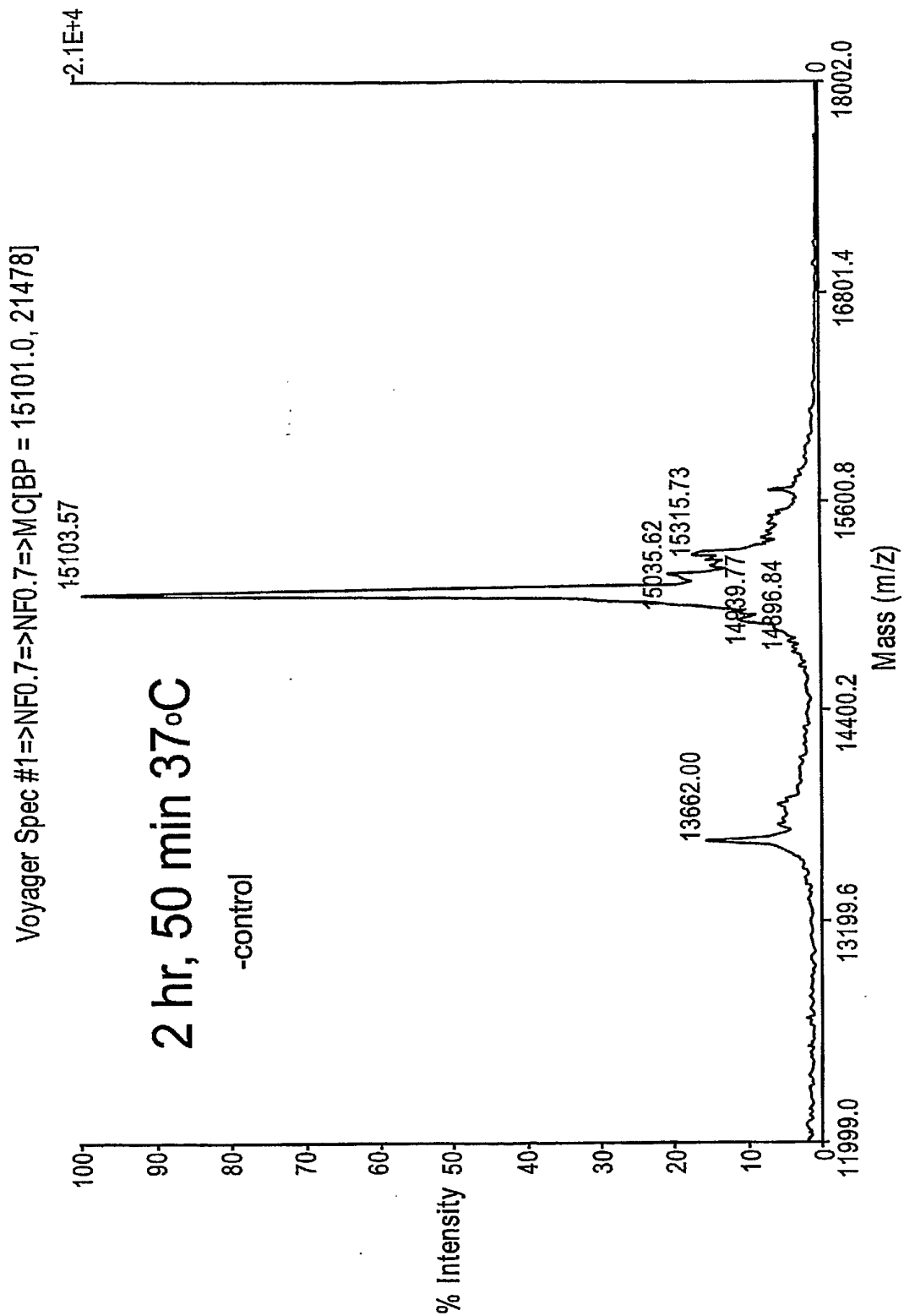


FIG. 33

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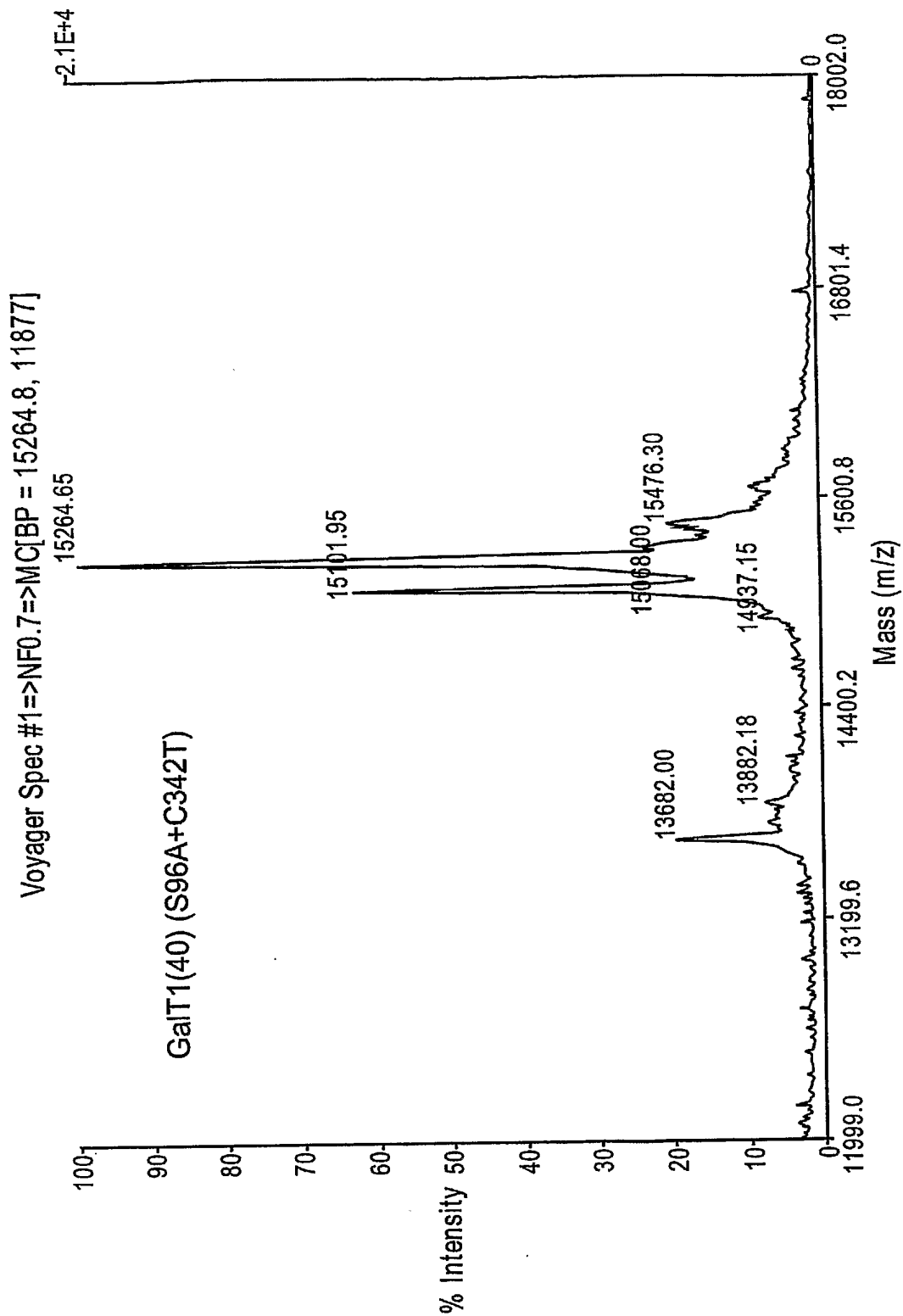


FIG. 33 (CONT.)

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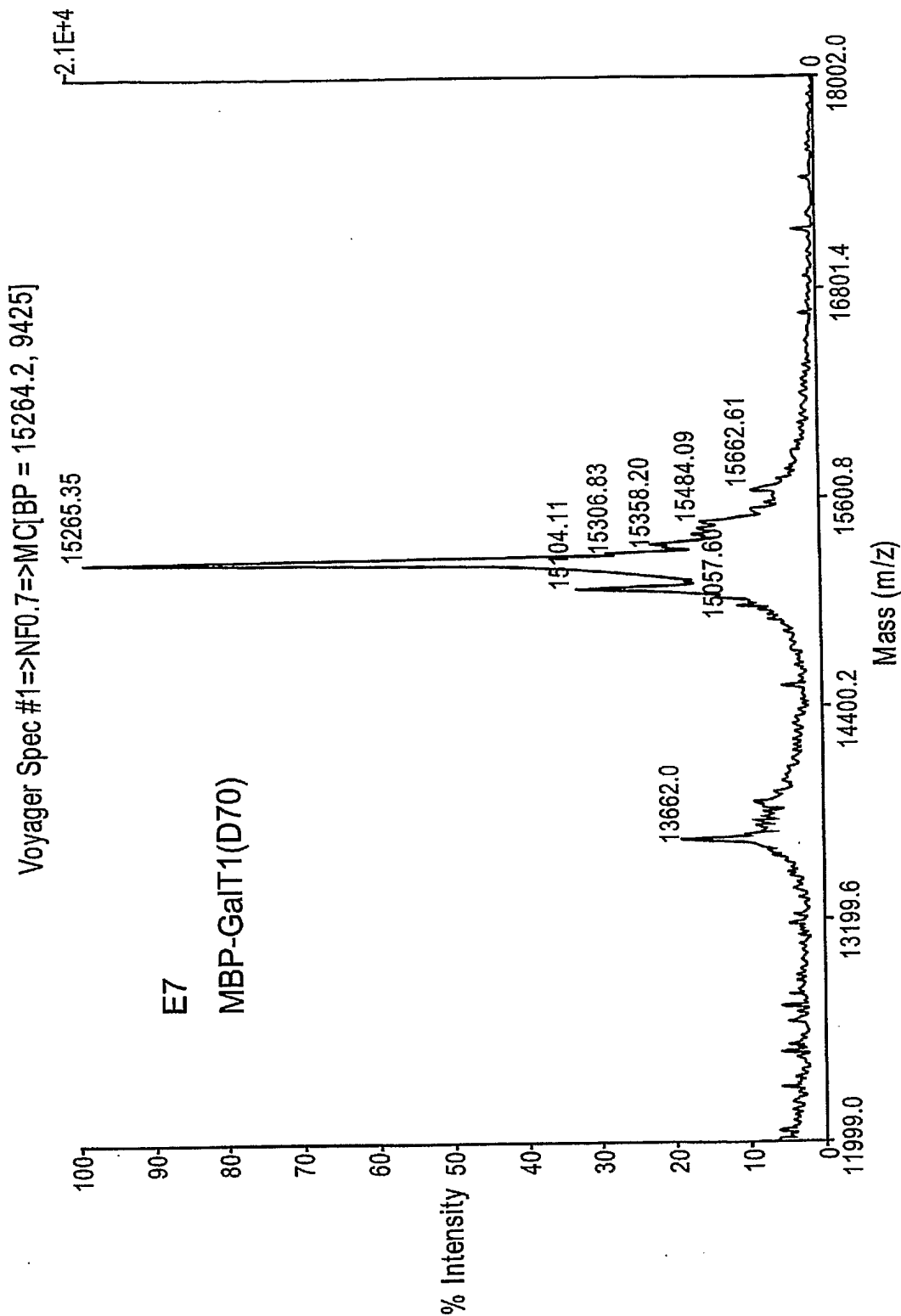


FIG. 33 (CONT.)

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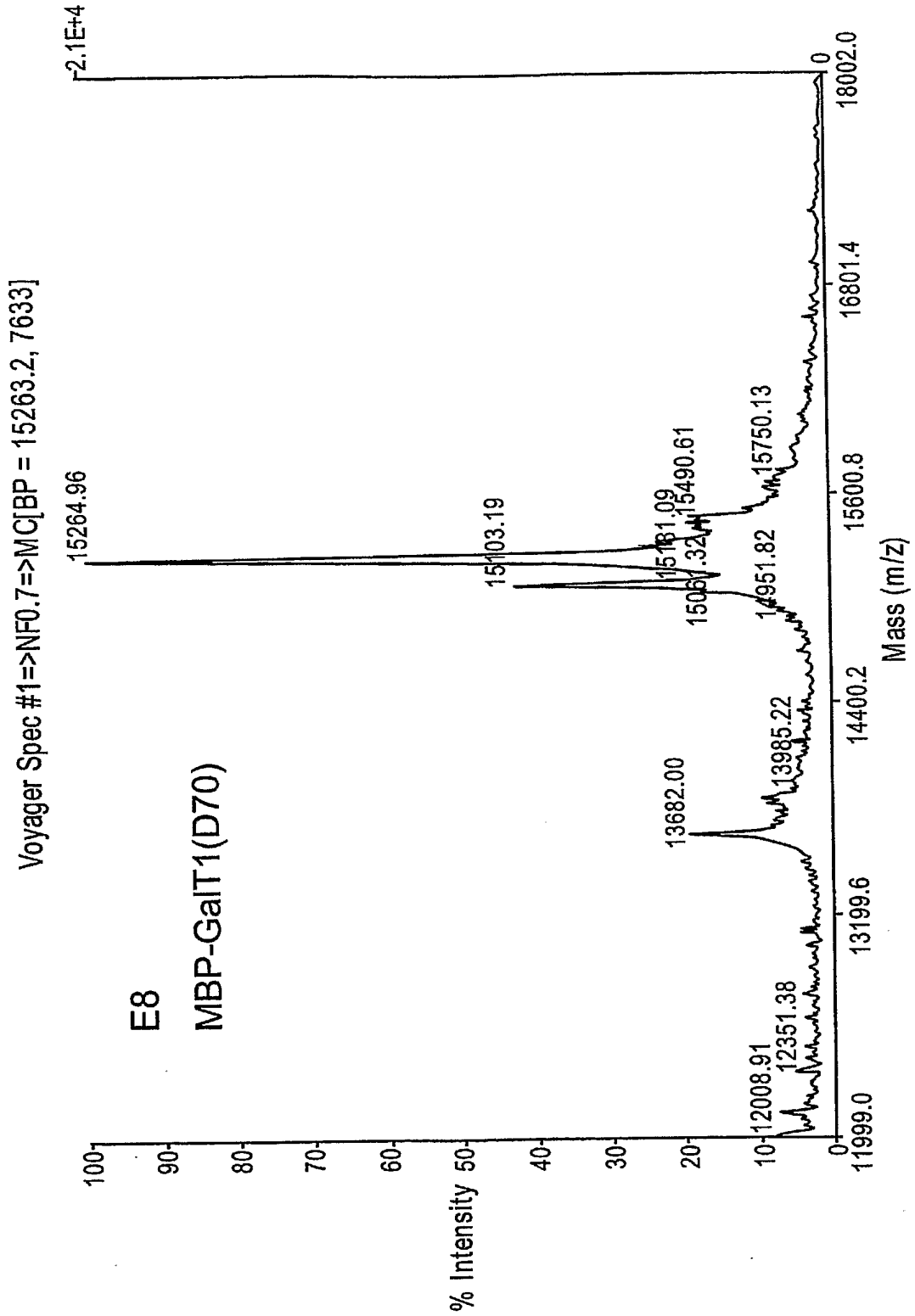


FIG. 33 (CONT.)

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Kinetics of RNase B modelling with GalT1 6.5.03

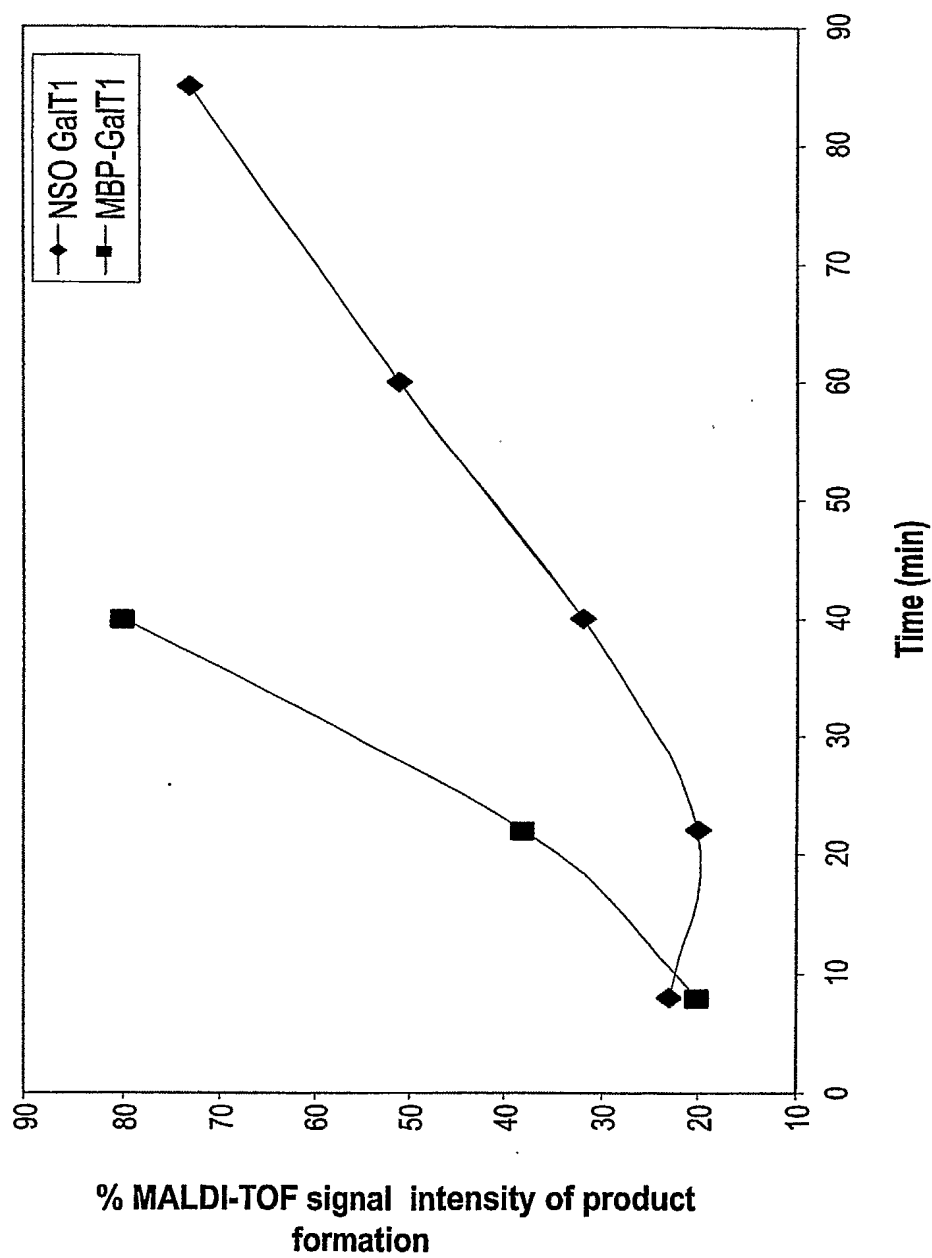
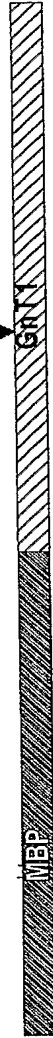


FIG. 34

GnT1 constructs

MBP-GnT1(Δ 35)

C121

MBP-GnT1(Δ 103)

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1 mlkksaglv lwgailfvaw nallllffwt rpapgrppsv saldgdpasl trevirlaqd
 61 aevelerqrg llqqigdals sqgrvrptaa ppagrvpvt papavipilv iacdrstvir
 121 clckllhyrp saelfpiivs qdcgheetaq aiasygsavt hirqpdlsi avppdhrkfq
 181 gyykiarhyr walgvvfrqf rfpaavvved dlevapdffe yfratypllk adpslwcvs
 241 wndngkeqmv dasrpellyr tdffpglgwl llaelwaele pkwpkafwdd wmrprpeqrg
 301 racirpeisr tmtfgrkgvs hggffdqhlk fiklngqfvh ftqldlsylq reaydrdfla
 361 rvygapqlqv ekvrtndrke lgevrvqytg rdsfkafaka lgvmdldksg vpragyrgiv
 421 tfqfgrgrrvh lappptwegy dpswn

FIG. 35

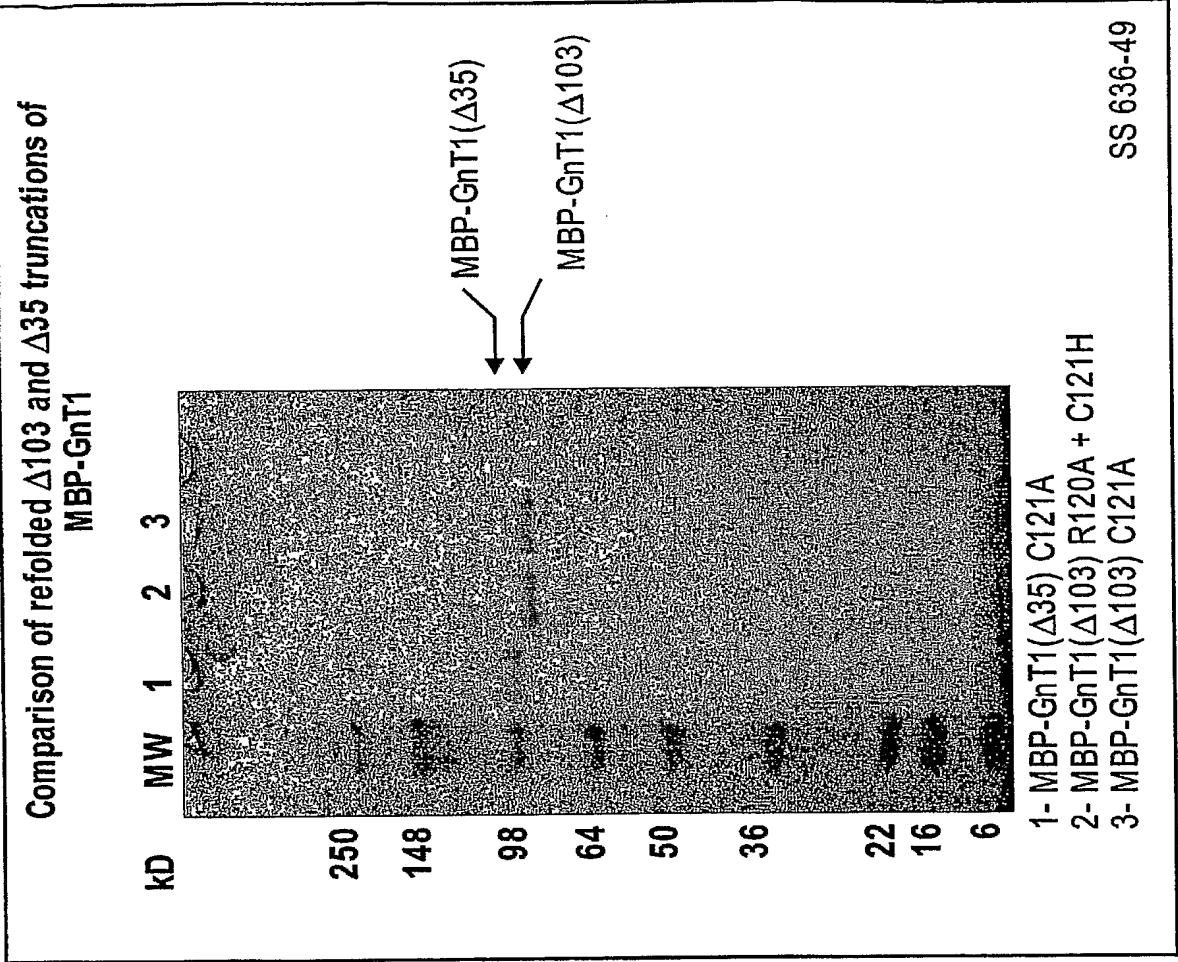
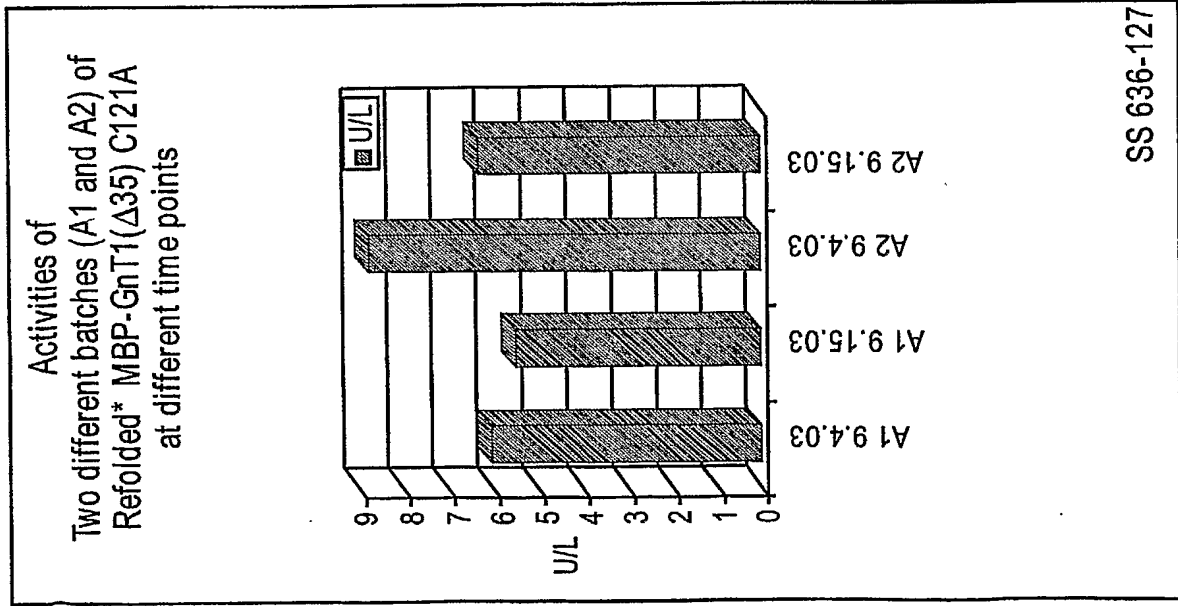


FIG. 36



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1 mapmrkkstl klltllvlfi fltsfflnys htvvttawfp kqmvielesen fkklmkypyr
61 pctctrciee qrvsawfder fnrsmqpllt aknahleedt ykwrlrlqre kqpnnlnndti
121 relfqvvp gn vdpallekrlv scrrcavvgn sgnlkesyvg pqidshdfvl rmnkaptgef
181 eadvgsktth hfvypesfre laqevsmilv pfkttidlewv isatttgts htyvpvpaki
241 kvkkekiliiy hpafikyvfd rwlqghgryp stgilsvifs lhicdevdly gfgadskgnw
301 hhywennpsa gafrktgvhd gdfesnvtti lasinkirif kgr

FIG. 37

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Human ST6GalNAcI

MRSCLWRCRHL SQGVQWSLL LAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQS
 LAKPKSQAPTRARRTTIYAEPVPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDK
 VPHTAQRAAWKSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQNG
 GQTRKLTASRTVSEKHQGAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIP
 PKEKKPQATPPPAPFQSPTTQRNQR LKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSV
 KIKASKSLWLQKLFLPNLTLFLDSRHFNQSEWDRLEHFAPPF GFMELNYSLVQKVVT
 RFPPVPQQQLLLASLPAGSLRCITCAVVGNGGILNNSHMGQEIDSHDYVFR LSGALIK
 GYEQDVGTRTSFYGFTAFSLTQSLLILGNRGFKNVPLGKDVRYLHFLEGRDYEWLE
 ALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLLHPDFLRYMKNRFLRSKTL D
 GAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHY YDTSWKRLIFYINH
 DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

FIG. 38A**Chicken ST6GalNAcI**

MGFLIRRLPKDSRIFRWLLILT VFSFIITSFSALFGMEKSIFRQLKIYQSI AHMLQVDTQ
 DQQGSNYSANGRISKVGLERDIAWLELNTAVSTPSGEGKEEQKKT VPKPAKVEEAK
 EKVTVKPFPEVMGITNTTASTASVVERTKEKT TARPVPGVGEADGKR TTIALPSMKE
 DKEKATVKPSFGMKVAHANSTSKDKPKAEPPASVKAIRPVTQAATVTEKKKLRAA
 DFKTEPQWDFDDEYILDSSSPVSTCSESVRAKAAKSDWLRDLFLPNITL FIDKSYFNV
 SEWDRLEHFAPPYGFME LNYSLVVEEVMSRLPPNPHQQLLANSSSNVSTCISCAVVG
 NGGILNNSGMGQEIDSHDYVFRVSGAVIKGYEKDVGT KTSFYGFTAYSLVSSLQNLG
 HKGFKKIPQGKHIRYIHFLEAVRDYEWL KALLLDKDIRKGFLNYYGRRPRERFDEDF
 TMNKYLVAHPDFLRYLKNRFLKSKNLQKPYWRLYRPTTGALLLLTALHLCDRV SAY
 GYITEGHQKYS DHYYDKEWKRLVFYVNHDFNLEKQVWKRLHDENIMKLYQRS

FIG. 38B

Mouse ST6GalNAcI protein beginning at residue 32 of the native mouse protein
 DPRAKDSRCQFIWKNDASAQENQQKAEPQVPIMTLSPRVHNKESTSVSSKDLKKQER
 EAVQGEQAEGKEKRKLETIRPAPENPQSKAEPAAKTPVSEHLDKLPRTPGALSTRKTP
 MATGAVPAKKKVQATKSPASSPHPTTRRRQRLKASEFKSEPRWDFEE EYSLDMSSL
 QTNCASV KIKASKSPWLQNIFLPNITLFLDSGRFTQSEWNRLEHFAPPF GFMELNQSL
 VQKVVT RFPPVRQQQLLLASLPTGYSKCITCAVVGNGGILNDSRVGREIDSHDYVFR
 LSGAVIKGYEQDVGTRTSFYGFTAFSLTQSILILGRRGFQHVPLGKDVRYLHFLEGR
 NYEWLEAMFLNQTLAKTHLSWFRHRPQEA FRNALDLDRYLLLHPDFLRYMKNRFL
 RSKTLDTAHWRIYRPTTGALLLLTALHLCDKVSAYGFITEGHQRFSDHY YDTSWKRL
 IFYINHDFRLERMVWKRLHDEGIWLYQR PQSDKAKN

FIG. 38C

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Hum (h)ST6GalNAcI truncations

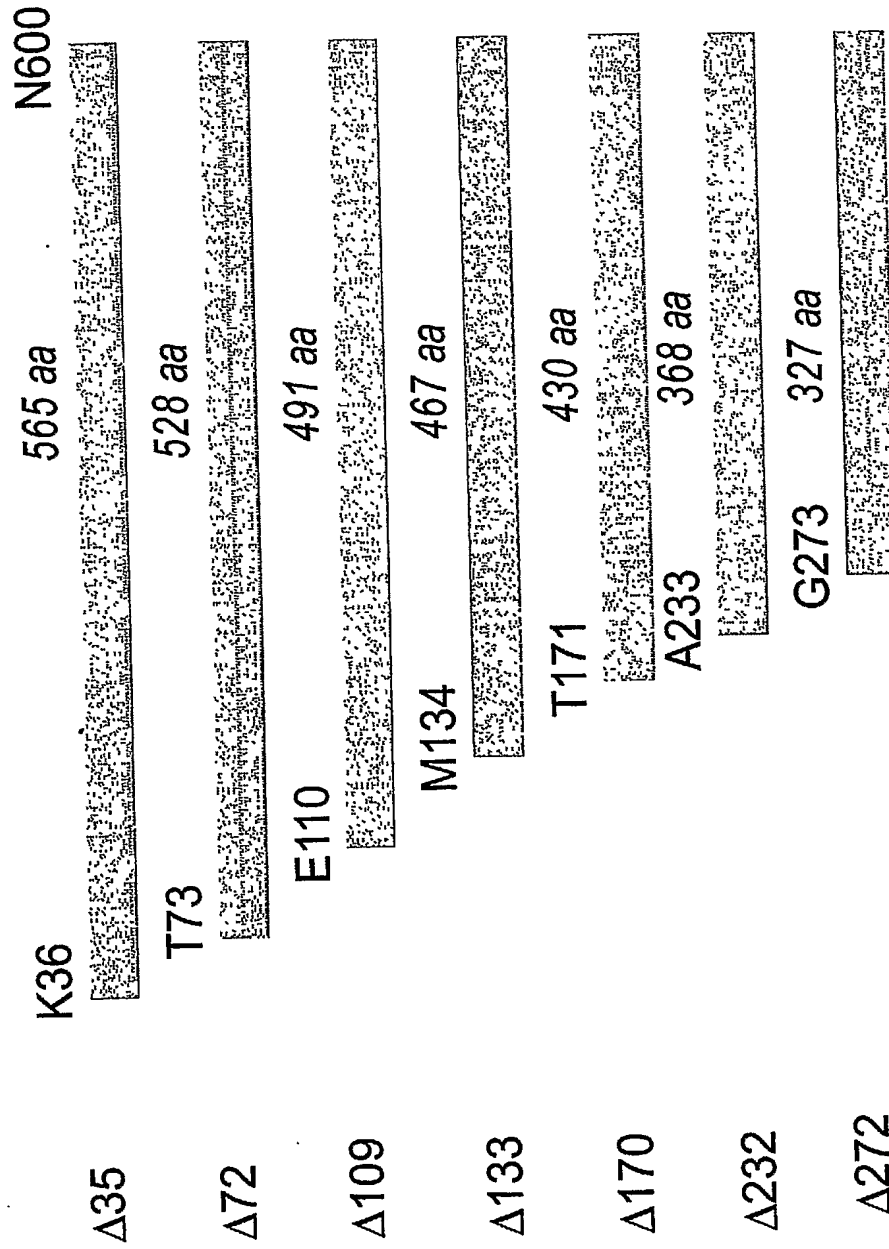


FIG. 39

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MBP-hST6GalNAc constructs

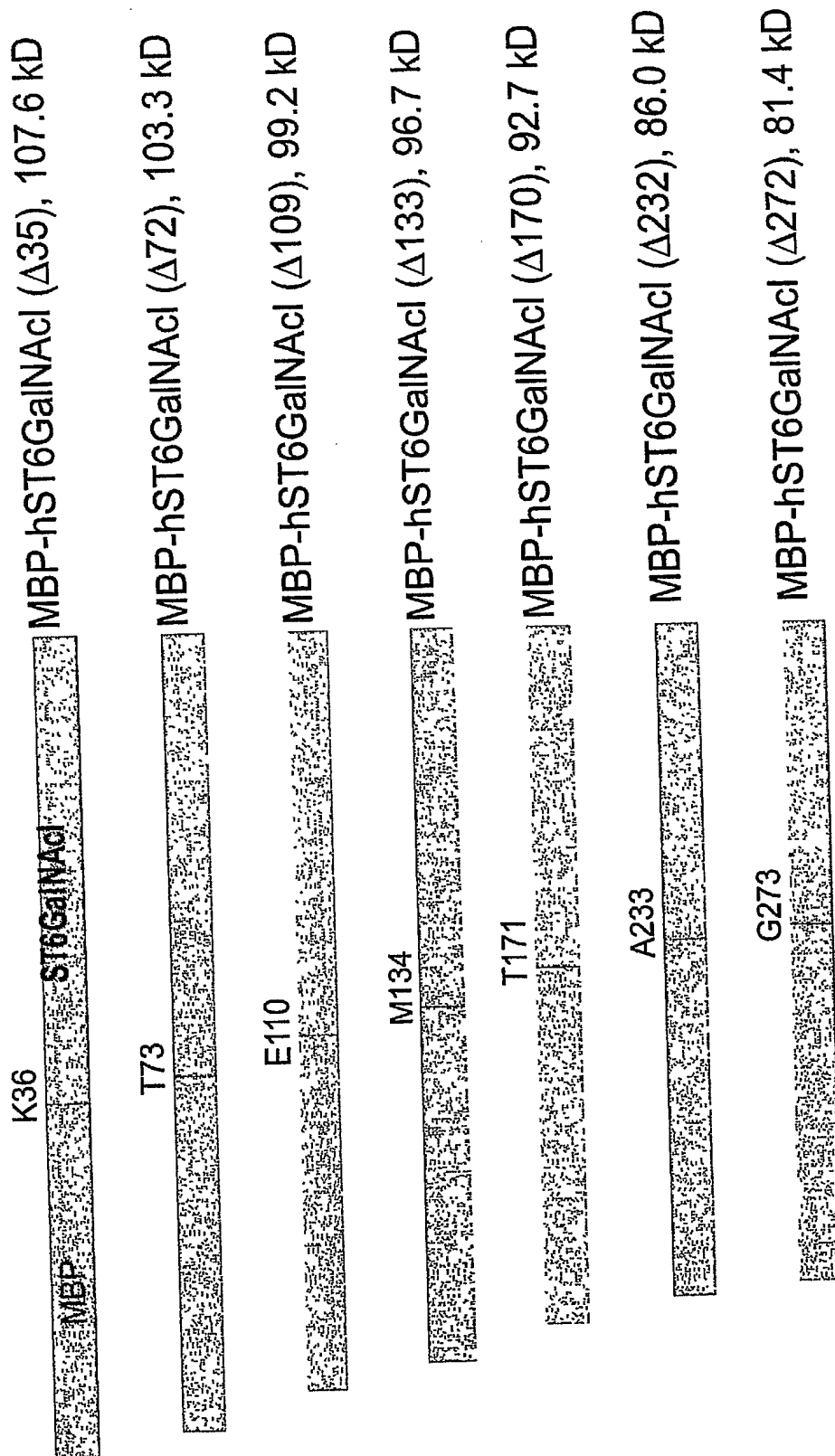


FIG. 40

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MASKSWLNFLTFLCGSAIGFLLCSQLFSILLGEKVDTQPNVLHNDPHARHSDDNGQN
HLEGQMNFNADSSQHKDENTDIAENLYQKVRILCWVMTGPQNLEKKAKHV KATW
AQRCNKVLFMSSEENKDFPAVGLKTKEGRDQLYWKTIKAFQYVHEHYLEDADWFL
KADDDTYVILDNLRWLLSKYDPEEPIYFGRRFKPYVKQGYMSGGAGYVLSKEALKR
FVDAFKTDKCTHSSSIEDLALGRCMEIMNVEAGDSRDTIGKETFHFPVPEHHLIKGYL
PRTFWYWNYNYYPPVEGPGCCSDLAVSFHYVDSTTMYELEYLVYHLRPYGYLYRY
QPTLPERILKEISQANKNEDTKVKLGNP

FIG. 41

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Yersinia MBP

MKIEEGKLV	WINGDKGYNG	LAEVGKKFEK	DTGIKVTIEH	PKLEEEKFPQ
VAATGDGPD	IFWAHDRFGG	YAQSGLLAEL	TPSKAFQEK	FPFTWDVAVR
NGKLIGYPVA	VEALSIIYNK	DLVKEAPKTW	EEIPALDKTL	RANGKSAIMW
NLQEPYFTWP	VIAADGGYAF	KEFENGVDYDAK	NVGVNNAGAQ	AGLQFIVDLV
KNKHINADTD	YSIAEAAFNK	GETAMTINGP	WAWSNIDKSK	INYGVTLLPT
FHGQPSKPFV	GVLTAGINAA	SPNKELATEF	LENYLITDQG	LAEVNKDKPL
GAVALKSQFQ	QLAKDPRIAA	TMDNATNGEI	MPNIPQMAAF	WYATRSVAVLN
AITGRQTVEA	ALNDAATRIT	K		

FIG. 43A*E. coli* MBP

MKIEEGKLV	WINGDKGYNG	LAEVGKKFEK	DTGIKVTVEH	PKLEEEKFPQ
VAATGDGPD	IFWAHDRFGG	YAQSGLLAEL	TPDKAFQDKL	YPFTWDVAVR
NGKLIAYPIA	VEALSIIYNK	DLLPNPPKTW	EEIPALDKEL	KAKGKSALMF
NLQEPYFTWP	LIAADGGYAF	KYENGKYDIK	DVGVDNAGAK	AGLTFLVDLI
KNKHMNADTD	YSIAEAAFNK	GETAMTINGP	WAWSNIDTSK	VNYGVTVLPT
FKGQPSKPFV	GVLSAGINAA	SPNKELAKEF	LENYLLTDEG	LEAVNKDKPL
GAVALKSYEE	ELAKDPRIAA	TMENAOQKEI	MPNIPQMSAF	WYAVRTAVIN
AASGRQTVDE	ALKDAQTNS			

FIG. 43B*Pyrococcus furiosus* MBP

MKIEEGKVVI	WHAMQPNELE	VFQSLAE EYM	ALSPEVEIVE	EQKPNLEDAL
KAAIPTGQGP	DLFIWAHDWI	GKFAEAGLLE	PIDEYVTEDL	LNEFAPMAQD
AMQYKGHYA	LPFAAETVAI	IYNKEMVSEP	PKTFDEMKA	MEKYYDPANE
KYGIAPWPIA	YFISAIQAQAF	GGYYFDDKTE	QPGLDKPETI	EGFKFFFTTEI
WPYMAPTGDY	NTQQSIFLEG	RAPMMVNGPW	SINDVKKAGI	NFGVVPLPPI
IKDGKEYWPR	PYGGVKLIYF	AAGIKNKDAA	WKFAKWLTS	EESIKTALAE
LGYIPVLTKV	LDDPEIKNDP	VIYGFQAVQ	HAYLMPKSPK	MSAVWGGVDG
AINEILQDPQ	NADIEGILKK	YQQEILNNMQ	G	

FIG. 43C*Thermococcus litoralis* MBP

MKIEEGKIVF	AVGGAPNEIE	YWKGVIAEFE	KKYPGVTVEL	KRQATDTEQR
RLDLVNALRG	KSSDPDVFLM	DVAWLGGQFIA	SGWLEPLDDY	VQKDNVDLSV
FFQSVINLAD	KQGGKLYALP	VYIDAGLLYY	RKDLLEKYGY	SKPPETWQEL
VEMAQKIQSG	ERETNPFWG	FVWQGGQYEG	LVCDFVEYVY	SNGGSLGEFK
DGKWVPTLNK	PENVEALQFM	VDLIHKYKIS	PPNTYTEMTE	EPVRLMFQQG
NAAFERNWPY	AWGLHNADDS	PVKGKVGVP	LPHFPGHKSA	ATLGGWHIGI
SKYSDNKALA	WEFVKFVESY	SVQKGFAMNL	GWNPGRVDVY	DDPAVVSQSP
HLKELRAVFE	NAVPRPIVPY	YPQLSEIIQK	YVNSALAGKI	SPQEALDKAQ
KEAEELVKQY	SK			

FIG. 43D*Thermatoga maritima* MBP

MKIEQTKLTI	WSSEKQVDIL	QKLGEFEKAK	YGIPVEVQYV	DEFSIKSKFL
TAAPQGGQAD	IIVGAHDWVG	ELAVNGLIEP	IPNFSDLKNF	YDTALKAFSY
GGKLYGVPIA	MEAVALIYNK	DYVDSVPKTM	DELIEKAKQI	DEEYGGGEVRG
FIYDVANFYF	SAPFILGYGG	YVFKETPQGL	DVTDIGLANE	GAVKGAKLIK
RMIDEGVLTP	GDNYGTMDSM	FKEGLAAMII	NGLWAIKSYK	DAGINYGVAP
IPELEPGVPA	KPFVGVQGF	INAKSPNKVI	AMEFLT NFIA	RKETMYKIYL
ADPRLPARKD	VLELVKDNPD	VVAFTQSASM	GTPMPNVPEM	APVWSAMGDA
LSIIINGQAS	VEDALKEAVD	KIKAQIEK		

FIG. 43E

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Vibrio cholerae MBP

MKIEEGQITI WINGDKGYNG LAEVGKKFEA DTGIKVTVAH PDALQDKFPQ
TAATGDGPD I VFWAHDREFGG YAEAGLLVEI KPSAKIQEGI VDFAWDAVKY
NGKIIGYPIA VESLSLIYNK DLVPNPPKSW EEVAELDAKL KKEGKSAIMW
NLKEPYFTWP LMAADGGYAF KYGVDGYDVK DAGINNKGVK DAMNEVKGLV
DKGVISPDMD YSVSESANQ GNTAMTINGP WSWGNIKSG INYGVTTLPK
FNGQASKPFV GVLTAGISTA SPNKDLAVEF IENYLLTNDG LRMVNNDKPL
GAVALNSFQR ELDADARIAA TMDNAMNGEI MPNIPQMNAF WSSAKNAIIN
IVDGRQTVDA ALADA EKQMT KP

FIG. 43F

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	1	50
HSGALNAT1.pep	(1)MRKFAYCKVVLATSLIWVLLDMFLLLYFS-----ECNKC	
HSGALNAT2.pep	(1)MRRRS--RMLLCFAFLWVLGIAYMYSGGGSALAGGAGGGAGRKEDWNEI	
Consensus	(1)MRK A KMLL A IWVL F L D N	
	51	100
HSGALNAT1.pep	(35)DEKKERGLPAGDVLEPVQKPHEGP-G-----EMGKPVVIPKEDQEKMKEM	
HSGALNAT2.pep	(49)DPIKKKDLHHSNGEKAQSMETLPPGKVRWPDFNQEAYVGGTMVRSGQDP	
Consensus	(51)D K K L E Q P G D I D	
	101	150
HSGALNAT1.pep	(79)FKINQENLMASEMIALNRSPLDVRLEGCKTKVYPDNLPTTSVVIVFHNEA	
HSGALNAT2.pep	(99)YARNKFNQVESDKLRMDRAIPDTRHDQCQRKQWRVDLPATSVVITFHNEA	
Consensus	(101)F N FN M SD I L RAIPD R D C K W LP TSVVI FHNEA	
	151	200
HSGALNAT1.pep	(129)WSTLLRTVHSVINSRPHMIEEIVLVDDASERDFLKRPLESYVKKLKVPV	
HSGALNAT2.pep	(149)RSALLRTVSVLKKSPPHLIKEIILVDDYSN-----DPEDGALLGKIEKV	
Consensus	(151) S LLRTV SVI KSP HLI EIILVDD S P D L V	
	201	250
HSGALNAT1.pep	(179)HVIRMEQRSGLIRARLKGA AVSKGQVITFLDAHCECTVGWLEPLIARIKH	
HSGALNAT2.pep	(194)RVLNRDRREGLMRSRVRGADAAQAKVLTFLDSHCECNEHWLEPLIERVAE	
Consensus	(201) VIR D R GLIRARLKGA A A VITFLDAHCEC WLEPLL RI	
	251	300
HSGALNAT1.pep	(229)DRRTVVCPIIDVISDDTFEYMAGSDMTYGGFNWKLNFRWYPVPQREMDRR	
HSGALNAT2.pep	(244)DRTRVVSPIIDVINMDNFQYVGASADLKGGFDWNLVFKWDYMTPEQRRSR	
Consensus	(251)DR VV PIIDVI D F YMAAS GGF W L FKW M R	
	301	350
HSGALNAT1.pep	(279)KGDRTL PVRTPTIMAGGLFSIDRDYFQEIGTYDAGMDIWGGENLEISFRIW	
HSGALNAT2.pep	(294)QGNPVAPIKTPTMIAGGLFVMDKFYFEELGKYDMMMDVWGGENLEISFRVW	
Consensus	(301) G PIKTP IAGGLF IDK YF EIG YD MDIWGGENLEISFRIW	
	351	400
HSGALNAT1.pep	(329)QCGGTLEIVTCSHVGHVFRKATPYTFPGGTGQIINKNNRRLAEVWMDEFK	
HSGALNAT2.pep	(344)QCGGSLEIIPCSRVGHVFRKQHPYTFPGSGTVFARNTRAAEVWMDEYK	
Consensus	(351)QCGGSLEII CS VGHVFRK PYTFPGSG I KN RR AEVWMDEFK	
	401	450
HSGALNAT1.pep	(379)NFFYIISPGVTKVDYGDISSRVGLRHKLQCKPFSWYLENIYPDSQIPRHY	
HSGALNAT2.pep	(394)NFFYAAVPSARNVPYGNIQSRLELRKKLSCKPFKWYLENVYPELRVPDHO	
Consensus	(401)NFFY P V YG I SRL LR KL CKPF WYLENIYPD IP H	
	451	500
HSGALNAT1.pep	(429)FSLGEIRNVEITNQCLDNMARKENEKVGIENCHGMGGNQVFSYTANKEIRT	
HSGALNAT2.pep	(444)DIAFGALQOGTN-CLDTLGHFADGVVGVYECHNAGGNQEWALTREKSVKH	
Consensus	(451) N TN CLD LA VGIF CH GGNQ FA T K IK	
	501	550
HSGALNAT1.pep	(479)DDLCLDVSKLN--GPVIMLKCHHLKGNQLWEYDPVKLTLOHVNSNQCLDK	
HSGALNAT2.pep	(493)MDLCLTVVDRAPGSLIKLQGCRENDSRQKWEQIEGNSKL RHVGSNLC LDS	
Consensus	(501) DLCL V I L C Q WE L HV SN CLD	
	551	584
HSGALNAT1.pep	(527)ATEEDSQVPSIRDCNGSRSSQOWLLRNVTLP EIF--	
HSGALNAT2.pep	(543)RTAK--SGGLSVEVCGPALSQOWKFTLNLOQ----	
Consensus	(551) T S SI C A SQOW	

FIG. 44

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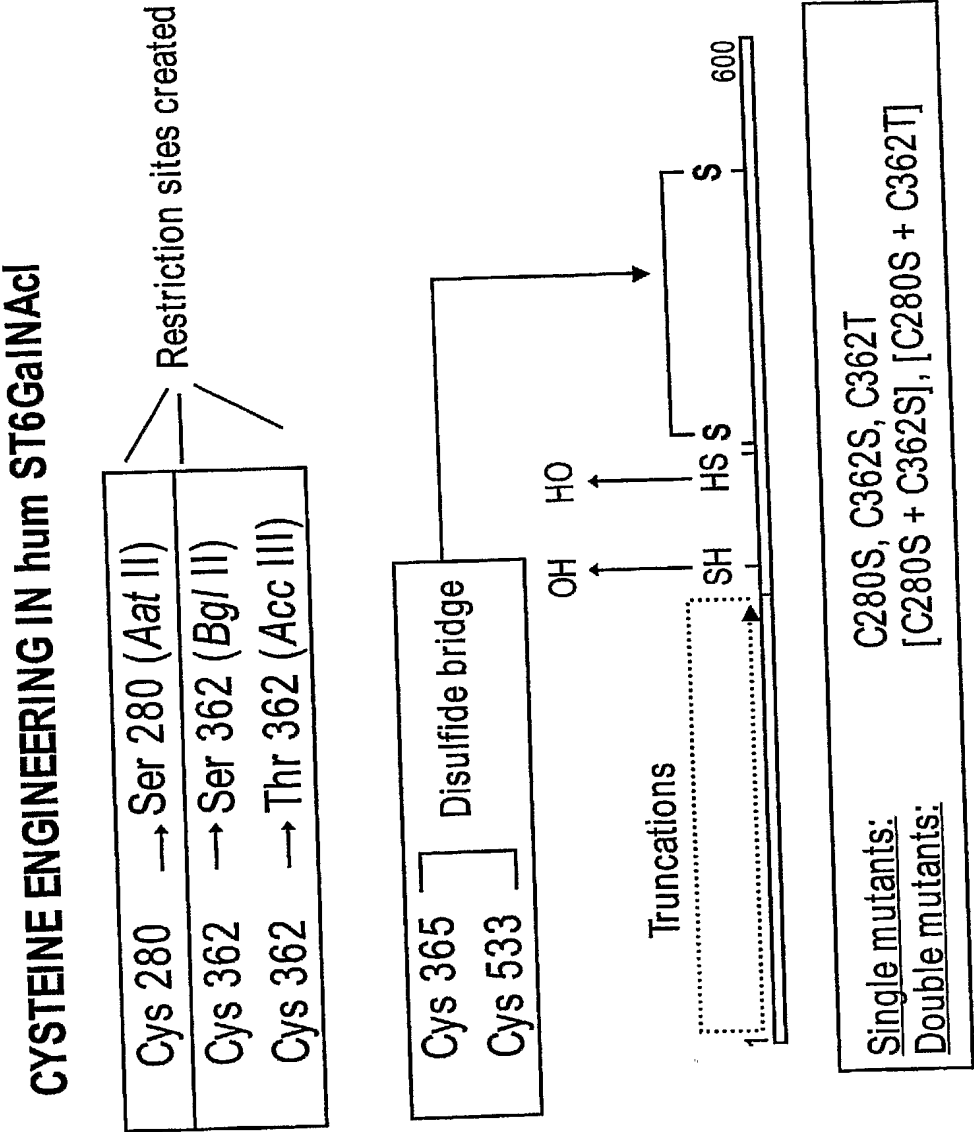


FIG. 45